

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 1, 2005, 08:40:57 ; Search time 23.793 Seconds
(without alignments)
1690.542 Million cell updates/sec

Title: US-10-624-932-2_COPY_495_598
Perfect score: 559
Sequence: 1 TSNMTYGTFFNFGRLMIPN.....CGEPSPDSWSLRLKKQSCEG 104

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_16Dec04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query		DB	ID	Description
		Match	Length			
1	559	100.0	437	4	AAB50690	Aab50690 Human HS1
2	559	100.0	544	7	ADG42581	Adg42581 Human tra
3	559	100.0	817	8	ADH71624	Adh71624 Human pro
4	559	100.0	833	8	ADH71622	Adh71622 Human pro
5	559	100.0	842	5	AAU74818	Aau74818 Human REP
6	559	100.0	842	8	ADL06574	Adl06574 Human tum
7	559	100.0	898	5	AAU85403	Aau85403 Human pro
8	559	100.0	898	5	AAU97899	Aau97899 Human net
9	559	100.0	898	8	ADH71618	Adh71618 Human pro

10	559	100.0	898	8	ADH71626	Adh71626	Human	pro
11	559	100.0	899	5	AAU79939	Aau79939	Human	UNC
12	559	100.0	899	7	ADG42569	Adg42569	Novel	hum
13	559	100.0	899	8	ADH71636	Adh71636	Human	pro
14	559	100.0	899	8	ADH71642	Adh71642	Human	pro
15	559	100.0	899	8	ADH71648	Adh71648	Human	pro
16	559	100.0	899	8	ADH71610	Adh71610	Human	pro
17	559	100.0	899	8	ADH71628	Adh71628	Human	pro
18	559	100.0	899	8	ADH71640	Adh71640	Human	pro
19	559	100.0	899	8	ADH71630	Adh71630	Human	pro
20	559	100.0	899	8	ADH71650	Adh71650	Human	pro
21	559	100.0	899	8	ADH71644	Adh71644	Human	pro
22	559	100.0	899	8	ADH71646	Adh71646	Human	pro
23	559	100.0	899	8	ADH71638	Adh71638	Human	pro
24	555	99.3	436	4	AAM25589	Aam25589	Human	pro
25	555	99.3	899	8	ADH71632	Adh71632	Human	pro
26	554	99.1	899	8	ADH71634	Adh71634	Human	pro
27	553	98.9	556	2	AAW78899	Aaw78899	Human	UNC
28	553	98.9	898	2	AAW78898	Aaw78898	Rat	UNC-5
29	553	98.9	898	5	AAU10543	Aau10543	Rat	netri
30	553	98.9	898	5	AAU97900	Aau97900	Rat	netri
31	548	98.0	898	7	ADG42580	Adg42580	Rat	trans
32	544	97.3	400	7	ADN95115	Adn95115	Human	LEC
33	465.5	83.3	943	4	AAM79128	Aam79128	Human	pro
34	347.5	62.2	266	4	AAB50650	Aab50650	Human	UNC
35	345	61.7	931	7	ADG42582	Adg42582	Mouse	tra
36	337	60.3	526	4	AAB50648	Aab50648	Human	UNC
37	337	60.3	931	4	AAB50691	Aab50691	Human	UNC
38	337	60.3	931	7	ADE63098	Ade63098	Human	Pro
39	337	60.3	931	7	ABU64297	Abu64297	Human	thr
40	337	60.3	931	8	ADR99258	Adr99258	Human	unc
41	337	60.3	964	8	ADR99250	Adr99250	Human	lRO
42	337	60.3	982	4	ABG11551	Abg11551	Novel	hum
43	334	59.7	931	7	ADG42584	Adg42584	Human	tra
44	322.5	57.7	929	7	ADG42583	Adg42583	Human	tra
45	318	56.9	238	4	AAB50646	Aab50646	Human	UNC

ALIGNMENTS

RESULT 1

AAB50690

ID AAB50690 standard; protein; 437 AA.

XX

AC AAB50690;

XX

DT 19-MAR-2001 (first entry)

XX

DE Human HS1 protein SEQ ID NO:89.

XX

KW Human; Caenorhabditis elegans; UNC-5; splice variant; nematode worm;
protein-protein interaction; identification.

XX

OS Homo sapiens.

XX

PN WO200073328-A2.

XX
 PD 07-DEC-2000.
 XX
 PF 02-JUN-2000; 2000WO-EP005108.
 XX
 PR 01-JUN-1999; 99GB-00012755.
 XX
 PA (DEVG-) DEVGEN NV.
 XX
 PI Van Crieckinge W, Roelens I, Bogaert T, Verwaerde P;
 XX
 DR WPI; 2001-016508/02.
 XX
 PT Three variants of human unc-5C cDNAs (unc-5Cb, unc-5Cc and unc-5C8) and a
 PT human unc-5HS1 cDNA, useful in yeast two hybrid experiments for
 PT identifying unknown human cDNAs which encode proteins that interact with
 PT the human unc-5C protein.
 XX
 PS Disclosure; Page 223-224; 246pp; English.
 XX
 CC The present invention describes 3 variants of human unc-5C cDNAs (unc-
 CC 5Cb, unc-5Cc and unc-5C8) which correspond to alternatively spliced unc-
 CC 5C transcripts, and a human unc-5HS1 cDNA which shares homology with the
 CC Rattus norvegicus unc-5HS1 cDNA. Also described are assays based on
 CC protein-protein-interactions between the unc-5 protein and a variety of
 CC different interacting proteins. The unc-5C variant cDNAs and unc-5HS1
 CC cDNA are useful in methods for identifying compounds which reduce or
 CC inhibit the lethal phenotype associated with the expression of the unc-5
 CC death domain in yeast. They are also useful in yeast two hybrid
 CC experiments for identifying unknown human cDNAs which encode proteins
 CC that interact with the human unc-5C protein. AAC90914 to AAC90971 and
 CC AAB50646 to AAB50693 represent sequences used in the exemplification of
 CC the present invention
 XX
 SQ Sequence 437 AA;

Query Match 100.0%; Score 559; DB 4; Length 437;
 Best Local Similarity 100.0%; Pred. No. 1.2e-57;
 Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TSNMTYGTFFNGLGGRIMIPNTGISLLIPPDAIPRGKIYEIYLT LHKPEDVRLPLAGCQTL 60
 |
 Db 34 TSNMTYGTFFNGLGGRIMIPNTGISLLIPPDAIPRGKIYEIYLT LHKPEDVRLPLAGCQTL 93
 Qy 61 LSPIVSCGPPGVLLTRPVILAMDHCGEPSDWSLRLKKQSCEG 104
 |
 Db 94 LSPIVSCGPPGVLLTRPVILAMDHCGEPSDWSLRLKKQSCEG 137

RESULT 2
 ADG42581
 ID ADG42581 standard; protein; 544 AA.
 XX
 AC ADG42581;
 XX
 DT 26-FEB-2004 (first entry)
 XX

DE Human transmembrane receptor Unc5H1 homologue.
 XX
 KW cytostatic; gene therapy; NOVX-agonist; NOVX-antagonist; pharmaceutical;
 KW NOVX-associated disorder; cancer; human; transmembrane receptor;
 KW Unc5H1 homologue.
 XX
 OS Homo sapiens.
 XX
 PN US2003204052-A1.
 XX
 PD 30-OCT-2003.
 XX
 PF 04-OCT-2001; 2001US-00970944.
 XX
 PR 04-OCT-2000; 2000US-0237862P.
 XX
 PA (HERR/) HERRMANN J L.
 PA (RAST/) RASTELLI L.
 PA (SHIM/) SHIMKETS R A.
 XX
 PI Herrmann JL, Rastelli L, Shimkets RA;
 XX
 DR WPI; 2003-900673/82.
 XX
 PT New NOVX gene or NOVX-specific antibody, useful for preparing a
 PT composition for treating or preventing a NOVX-associated disorder, e.g.,
 PT cancer.
 XX
 PS Disclosure; SEQ ID NO 14; 118pp; English.
 XX
 CC The invention describes a new isolated polypeptide comprising: a
 CC polypeptide or its mature form comprising a sequence not given in the
 CC specification; or a variant of (A), where one or more amino acid residues
 CC in the variant differs in no more than 15% from the amino acid sequence
 CC of the mature form. The pharmaceutical composition may be administered
 CC via oral, transdermal, rectal or parenteral route. The polypeptide,
 CC nucleic acid or antibody is useful for preparing a composition for
 CC treating or preventing a NOVX-associated disorder, e.g., cancer. This is
 CC the amino acid sequence of a transmembrane receptor homologue used in a
 CC comparison with the novel human proteins of the invention.
 XX
 SQ Sequence 544 AA;

Query Match 100.0%; Score 559; DB 7; Length 544;
 Best Local Similarity 100.0%; Pred. No. 1.6e-57;
 Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TSNMTYGTFFNLGGRLMIPNTGISLLIPDAIPRGKIYEIYLTLLHKPEDVRLPLAGCQTL 60
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 141 TSNMTYGTFFNLGGRLMIPNTGISLLIPDAIPRGKIYEIYLTLLHKPEDVRLPLAGCQTL 200
 Qy 61 LSPIVSCGPPGVLLTRPVILAMDHCGEPSDPSWSLRLKKQSCEG 104
 ||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 201 LSPIVSCGPPGVLLTRPVILAMDHCGEPSDPSWSLRLKKQSCEG 244

RESULT 3

ADH71624

ID ADH71624 standard; protein; 817 AA.

XX

AC ADH71624;

XX

DT 25-MAR-2004 (first entry)

XX

DE Human protein of the invention NOV21h SEQ ID NO:520.

XX

KW human; cytostatic; immunomodulator; neuroprotective; nootropic;
KW anorectic; antidiabetic; antimicrobial; antilipaemic; gene therapy;
KW vaccine; cancer; cachexia; Alzheimer's disease; Parkinson's disease;
KW obesity; diabetes; infectious disease; metabolic syndrome X;
KW dyslipidaemia.

XX

OS Homo sapiens.

XX

PN WO2003102155-A2.

XX

PD 11-DEC-2003.

XX

PF 03-JUN-2003; 2003WO-US017430.

XX

PR 03-JUN-2002; 2002US-0385120P.

PR 04-JUN-2002; 2002US-0385784P.

PR 05-JUN-2002; 2002US-0386041P.

PR 05-JUN-2002; 2002US-0386047P.

PR 06-JUN-2002; 2002US-0386376P.

PR 06-JUN-2002; 2002US-0386453P.

PR 06-JUN-2002; 2002US-0386864P.

PR 06-JUN-2002; 2002US-0387016P.

PR 07-JUN-2002; 2002US-0386796P.

PR 07-JUN-2002; 2002US-0386816P.

PR 07-JUN-2002; 2002US-0386931P.

PR 07-JUN-2002; 2002US-0386942P.

PR 07-JUN-2002; 2002US-0386971P.

PR 07-JUN-2002; 2002US-0387262P.

PR 08-JUN-2002; 2002US-0296960P.

PR 10-JUN-2002; 2002US-0387400P.

PR 10-JUN-2002; 2002US-0387535P.

PR 11-JUN-2002; 2002US-0387610P.

PR 11-JUN-2002; 2002US-0387625P.

PR 11-JUN-2002; 2002US-0387634P.

PR 11-JUN-2002; 2002US-0387668P.

PR 11-JUN-2002; 2002US-0387696P.

PR 11-JUN-2002; 2002US-0387702P.

PR 11-JUN-2002; 2002US-0387836P.

PR 11-JUN-2002; 2002US-0387859P.

PR 12-JUN-2002; 2002US-0387933P.

PR 12-JUN-2002; 2002US-0387934P.

PR 12-JUN-2002; 2002US-0387960P.

PR 12-JUN-2002; 2002US-0388022P.

PR 12-JUN-2002; 2002US-0388096P.

PR 13-JUN-2002; 2002US-0389123P.

PR 14-JUN-2002; 2002US-0389118P.

PR 14-JUN-2002; 2002US-0389120P.

PR 14-JUN-2002; 2002US-0389144P.

PR 14-JUN-2002; 2002US-0389146P.
PR 17-JUN-2002; 2002US-0389729P.
PR 17-JUN-2002; 2002US-0389742P.
PR 18-JUN-2002; 2002US-0389884P.
PR 19-JUN-2002; 2002US-0390006P.
PR 19-JUN-2002; 2002US-0390209P.
PR 21-JUN-2002; 2002US-0390763P.
PR 17-JUL-2002; 2002US-0396706P.
PR 06-AUG-2002; 2002US-0401628P.
PR 09-AUG-2002; 2002US-0402156P.
PR 09-AUG-2002; 2002US-0402256P.
PR 09-AUG-2002; 2002US-0402389P.
PR 12-AUG-2002; 2002US-0402786P.
PR 12-AUG-2002; 2002US-0402816P.
PR 12-AUG-2002; 2002US-0402821P.
PR 12-AUG-2002; 2002US-0402832P.
PR 13-AUG-2002; 2002US-0403448P.
PR 13-AUG-2002; 2002US-0403459P.
PR 13-AUG-2002; 2002US-0403531P.
PR 13-AUG-2002; 2002US-0403532P.
PR 13-AUG-2002; 2002US-0403563P.
PR 13-AUG-2002; 2002US-0406317P.
PR 15-AUG-2002; 2002US-0403617P.
PR 26-AUG-2002; 2002US-0406182P.
PR 26-AUG-2002; 2002US-0406355P.
PR 27-AUG-2002; 2002US-0406240P.
PR 12-SEP-2002; 2002US-0410084P.
PR 20-SEP-2002; 2002US-0412528P.
PR 23-SEP-2002; 2002US-0412731P.
PR 30-SEP-2002; 2002US-0414801P.
PR 30-SEP-2002; 2002US-0414839P.
PR 30-SEP-2002; 2002US-0414840P.
PR 30-SEP-2002; 2002US-0414954P.
PR 09-OCT-2002; 2002US-0417186P.
PR 09-OCT-2002; 2002US-0417406P.
PR 23-OCT-2002; 2002US-0420639P.
PR 28-OCT-2002; 2002US-0421156P.
PR 31-OCT-2002; 2002US-0422690P.
PR 01-NOV-2002; 2002US-0423130P.
PR 05-NOV-2002; 2002US-00423798.
PR 05-NOV-2002; 2002US-0423798P.
PR 12-NOV-2002; 2002US-0425453P.

XX

PA (CURA-) CURAGEN CORP.

XX

PI Alsobrook JP, Alvarez E, Anderson DW, Boldog FL, Casman SJ;
PI Catterton E, Chapoval A, Crabtree-Bokor JR, Edinger SR, Ellerman K;
PI Ettenberg S, Gangolli EA, Gerlach VL, Gorman L, Gunther E, Guo X;
PI Gusev VY, Herrmann JL, Ji W, Kekuda R, Li L, Liu X, Macdougall JR;
PI Maclachlan T, Malyankar UM, Mezick AJ, Millet I, Mishra VS;
PI Padigar M, Patturajan M, Pena CEA, Peyman JA, Raha D, Rastelli L;
PI Rieger DK, Rothenberg ME, Sciore P, Shenoy SG, Shimkets RA;
PI Smithson G, Spytek KA, Stone DJ, Vernet CAM, Voss EZ, Zhong M;
PI Zhong H;

XX

DR WPI; 2004-081935/08.

DR N-PSDB; ADH71623.

XX
PD 11-DEC-2003.
XX
PF 03-JUN-2003; 2003WO-US017430.
XX
PR 03-JUN-2002; 2002US-0385120P.
PR 04-JUN-2002; 2002US-0385784P.
PR 05-JUN-2002; 2002US-0386041P.
PR 05-JUN-2002; 2002US-0386047P.
PR 06-JUN-2002; 2002US-0386376P.
PR 06-JUN-2002; 2002US-0386453P.
PR 06-JUN-2002; 2002US-0386864P.
PR 06-JUN-2002; 2002US-0387016P.
PR 07-JUN-2002; 2002US-0386796P.
PR 07-JUN-2002; 2002US-0386816P.
PR 07-JUN-2002; 2002US-0386931P.
PR 07-JUN-2002; 2002US-0386942P.
PR 07-JUN-2002; 2002US-0386971P.
PR 07-JUN-2002; 2002US-0387262P.
PR 08-JUN-2002; 2002US-0296960P.
PR 10-JUN-2002; 2002US-0387400P.
PR 10-JUN-2002; 2002US-0387535P.
PR 11-JUN-2002; 2002US-0387610P.
PR 11-JUN-2002; 2002US-0387625P.
PR 11-JUN-2002; 2002US-0387634P.
PR 11-JUN-2002; 2002US-0387668P.
PR 11-JUN-2002; 2002US-0387696P.
PR 11-JUN-2002; 2002US-0387702P.
PR 11-JUN-2002; 2002US-0387836P.
PR 11-JUN-2002; 2002US-0387859P.
PR 12-JUN-2002; 2002US-0387933P.
PR 12-JUN-2002; 2002US-0387934P.
PR 12-JUN-2002; 2002US-0387960P.
PR 12-JUN-2002; 2002US-0388022P.
PR 12-JUN-2002; 2002US-0388096P.
PR 13-JUN-2002; 2002US-0389123P.
PR 14-JUN-2002; 2002US-0389118P.
PR 14-JUN-2002; 2002US-0389120P.
PR 14-JUN-2002; 2002US-0389144P.
PR 14-JUN-2002; 2002US-0389146P.
PR 17-JUN-2002; 2002US-0389729P.
PR 17-JUN-2002; 2002US-0389742P.
PR 18-JUN-2002; 2002US-0389884P.
PR 19-JUN-2002; 2002US-0390006P.
PR 19-JUN-2002; 2002US-0390209P.
PR 21-JUN-2002; 2002US-0390763P.
PR 17-JUL-2002; 2002US-0396706P.
PR 06-AUG-2002; 2002US-0401628P.
PR 09-AUG-2002; 2002US-0402156P.
PR 09-AUG-2002; 2002US-0402256P.
PR 09-AUG-2002; 2002US-0402389P.
PR 12-AUG-2002; 2002US-0402786P.
PR 12-AUG-2002; 2002US-0402816P.
PR 12-AUG-2002; 2002US-0402821P.
PR 12-AUG-2002; 2002US-0402832P.
PR 13-AUG-2002; 2002US-0403448P.
PR 13-AUG-2002; 2002US-0403459P.

PR 13-AUG-2002; 2002US-0403531P.
PR 13-AUG-2002; 2002US-0403532P.
PR 13-AUG-2002; 2002US-0403563P.
PR 13-AUG-2002; 2002US-0406317P.
PR 15-AUG-2002; 2002US-0403617P.
PR 26-AUG-2002; 2002US-0406182P.
PR 26-AUG-2002; 2002US-0406355P.
PR 27-AUG-2002; 2002US-0406240P.
PR 12-SEP-2002; 2002US-0410084P.
PR 20-SEP-2002; 2002US-0412528P.
PR 23-SEP-2002; 2002US-0412731P.
PR 30-SEP-2002; 2002US-0414801P.
PR 30-SEP-2002; 2002US-0414839P.
PR 30-SEP-2002; 2002US-0414840P.
PR 30-SEP-2002; 2002US-0414954P.
PR 09-OCT-2002; 2002US-0417186P.
PR 09-OCT-2002; 2002US-0417406P.
PR 23-OCT-2002; 2002US-0420639P.
PR 28-OCT-2002; 2002US-0421156P.
PR 31-OCT-2002; 2002US-0422690P.
PR 01-NOV-2002; 2002US-0423130P.
PR 05-NOV-2002; 2002US-00423798.
PR 05-NOV-2002; 2002US-0423798P.
PR 12-NOV-2002; 2002US-0425453P.

XX

PA (CURA-) CURAGEN CORP.

XX

PI Alsobrook JP, Alvarez E, Anderson DW, Boldog FL, Casman SJ;
PI Catterton E, Chapoval A, Crabtree-Bokor JR, Edinger SR, Ellerman K;
PI Ettenberg S, Gangolli EA, Gerlach VL, Gorman L, Gunther E, Guo X;
PI Gusev VY, Herrmann JL, Ji W, Kekuda R, Li L, Liu X, Macdougall JR;
PI Maclachlan T, Malyankar UM, Mezick AJ, Millet I, Mishra VS;
PI Padigar M, Patturajan M, Pena CEA, Peyman JA, Raha D, Rastelli L;
PI Rieger DK, Rothenberg ME, Sciore P, Shenoy SG, Shimkets RA;
PI Smithson G, Spytek KA, Stone DJ, Vernet CAM, Voss EZ, Zhong M;
PI Zhong H;

XX

DR WPI; 2004-081935/08.

DR N-PSDB; ADH71621.

XX

PT New NOVX polypeptides and nucleic acid molecules useful for preventing or
PT treating NOVX-associated disorders, e.g. cancer, diabetes, infection or
PT obesity, and in chromosome mapping, tissue typing or pharmacogenomics.

XX

PS Example 21; SEQ ID NO 518; 1880pp; English.

XX

CC The invention relates to a novel isolated polypeptide (NOVX). A
CC polypeptide of the invention has cytostatic, immunomodulator,
CC neuroprotective, nootropic, anorectic, antidiabetic, antimicrobial, and
CC antilipaemic activity, and may have a use in gene therapy, and as a
CC vaccine. The polypeptides are encoded by NOVX polynucleotides comprising
CC any of the 303 fully defined nucleotide sequences given in the
CC specification. The polypeptide is useful in the manufacture of a
CC medicament for treating a syndrome associated with a human disease. The
CC polypeptide, polynucleotide and antibody are useful in diagnosing,
CC treating or preventing NOVX-associated disorders, e.g. cancer, cachexia,
CC Alzheimer's disease, Parkinson's disease, obesity, diabetes, infectious

XX
 DT 20-MAY-2004 (first entry)
 XX
 DE Human tumour-associated antigenic target (TAT) polypeptide #73.
 XX
 KW Human; tumour-associated antigenic target; TAT; cell death; tumour;
 KW cancer; cytostatic.
 XX
 OS Homo sapiens.
 XX
 PN WO2004016225-A2.
 XX
 PD 26-FEB-2004.
 XX
 PF 19-AUG-2003; 2003WO-US025892.
 XX
 PR 19-AUG-2002; 2002US-0404809P.
 PR 21-AUG-2002; 2002US-0405645P.
 PR 23-SEP-2002; 2002US-0413192P.
 PR 15-OCT-2002; 2002US-0419008P.
 PR 15-NOV-2002; 2002US-0426847P.
 PR 02-JUL-2003; 2003US-0484959P.
 XX
 PA (GETH) GENENTECH INC.
 XX
 PI Desauvage FJ, Frantz G, Hillan KJ, Polakis P, Polson A, Smith V;
 PI Spencer SD, Wu TD, Zhang Z;
 XX
 DR WPI; 2004-257144/24.
 DR N-PSDB; ADL06497.
 XX
 PT New antibody that binds to a tumor-associated antigenic target (TAT)
 PT polypeptide, useful for preparing a composition for diagnosing or
 PT treating cancer.
 XX
 PS Claim 2; SEQ ID NO 154; 319pp; English.
 XX
 CC The present invention relates to the isolation of human tumour-associated
 CC antigenic target (TAT) polynucleotide and polypeptide sequences. Also
 CC disclosed is an antibody that binds to a TAT polypeptide. The antibody is
 CC a monoclonal antibody, an antibody fragment, a chimeric antibody or a
 CC humanised antibody. It is conjugated to a growth inhibitory agent. It is
 CC produced in bacteria or in CHO cells and induces death of a cell to which
 CC it binds. The antibody is useful for preparing a composition for
 CC diagnosing or treating tumours and cancer. The present sequence
 CC represents a human TAT polypeptide of the invention.
 XX
 SQ Sequence 842 AA;

Query Match 100.0%; Score 559; DB 8; Length 842;
 Best Local Similarity 100.0%; Pred. No. 2.8e-57;
 Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TSNMTYGTFFNLGGRLMIPNTGISLLIPPDAIPRGKIYEIYLT LHKPEDVRLPLAGCQTL 60
 ||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 439 TSNMTYGTFFNLGGRLMIPNTGISLLIPPDAIPRGKIYEIYLT LHKPEDVRLPLAGCQTL 498

Qy 61 LSPIVSCGPPGVLLTRPVILAMDHCGEPSDWSLRLKKQSCEG 104
|||||
Db 499 LSPIVSCGPPGVLLTRPVILAMDHCGEPSDWSLRLKKQSCEG 542

RESULT 7

AAU85403

ID AAU85403 standard; protein; 898 AA.

XX

AC AAU85403;

XX

DT 21-MAY-2002 (first entry)

XX

DE Human protein NOV1.

XX

KW Human; NOVX; cardiomyopathy; atherosclerosis; diabetes;

KW cell signal processing disorder; metabolic disorder; obesity; infection;

KW anorexia; cancer-associated cachexia; cancer; neurodegenerative disorder;

KW Alzheimer's disease; Parkinson's disease; immune disorder;

KW haematopoietic disorders; dyslipidaemia; pain; asthma; hypertension;

KW osteoporosis; Crohn's disease; multiple sclerosis; angina pectoris;

KW myocardial infarction; ulcer; allergy; benign prostatic hypertrophy;

KW psychosis; neurological disorder; anxiety; schizophrenia;

KW manic depression; dementia; dyskinesia; Huntington's disease;

KW Gilles de la Tourette's syndrome; gene therapy.

XX

OS Homo sapiens.

XX

PN WO200210216-A2.

XX

PD 07-FEB-2002.

XX

PF 30-JUL-2001; 2001WO-US024225.

XX

PR 28-JUL-2000; 2000US-0221409P.

PR 04-AUG-2000; 2000US-0222840P.

PR 04-AUG-2000; 2000US-0223752P.

PR 04-AUG-2000; 2000US-0223762P.

PR 04-AUG-2000; 2000US-0223769P.

PR 04-AUG-2000; 2000US-0223770P.

PR 14-AUG-2000; 2000US-0225146P.

PR 15-AUG-2000; 2000US-0225392P.

PR 15-AUG-2000; 2000US-0225470P.

PR 16-AUG-2000; 2000US-0225697P.

PR 01-FEB-2001; 2001US-0263662P.

PR 05-APR-2001; 2001US-0281645P.

XX

PA (CURA-) CURAGEN CORP.

XX

PI Padigar M, Mezes P, Mishra V, Burgess C, Casman S, Grosse WM;

PI Alsobrook JP, Lepley DM, Gerlach VL, Macdougall JR, Smithson G;

XX

DR WPI; 2002-180074/23.

DR N-PSDB; ABK37922.

XX

PT New isolated cytoplasmic, nuclear, membrane bound, or secreted

PT polypeptide, useful for treating cardiomyopathy, atherosclerosis,

KW multiple sclerosis; Alzheimer's disease.

XX

OS Homo sapiens.

XX

FH Key Location/Qualifiers

FT Domain 152. .223

FT /note= "Immunoglobulin domain "

FT Domain 247. .294

FT /note= "Thrombospondine type 1 domain "

FT Domain 302. .348

FT /note= "Thrombospondine type 1 domain"

FT Region 361. .382

FT /note= "Transmembrane region"

FT Domain 495. .598

FT /note= "ZU5 domain"

FT Domain 817. .897

FT /note= "Death domain"

XX

PN WO200233080-A2.

XX

PD 25-APR-2002.

XX

PF 15-OCT-2001; 2001WO-EP011891.

XX

PR 16-OCT-2000; 2000US-0240061P.

XX

PA (FARB) BAYER AG.

XX

PI Koehler RH;

XX

DR WPI; 2002-463314/49.

DR N-PSDB; ABK52891.

XX

PT Novel human netrin binding membrane receptor polypeptide and
PT polynucleotides for identifying modulating agents useful in treating
PT diseases e.g. Parkinson's disease, multiple sclerosis, stroke,
PT Alzheimer's disease.

XX

PS Claim 1; Fig 2; 94pp; English.

XX

CC This invention relates to the DNA and protein sequences of a novel
CC purified human netrin binding membrane receptor, UNC5H-1. The DNA
CC sequence of the invention is useful as a probe for detecting a nucleic
CC acid encoding the UNC5H-1 protein in a biological sample. The sequences
CC of the invention are useful to screen for agents which decrease the
CC activity of the UNC5H-1 protein. The sequences are also useful for
CC screening agents which regulate (modulate) the activity of the protein of
CC the invention. A pharmaceutical composition containing the protein of the
CC invention or a reagent that modulates the activity of the UNC5H-1 protein
CC may be useful for treating a UNC5H-1 dysfunction related disease such as
CC cancer or a central nervous system (CNS) disorders (e.g, Parkinson's
CC disease, multiple sclerosis, stroke and Alzheimer's disease). Fusion
CC proteins comprising the UNC5H-1 protein are useful for generating
CC antibodies and for in various assay systems, and the protein can be used
CC as a bait protein in a two-hybrid assay or three-hybrid assay. The method
CC of the invention is useful for detecting a coding sequence for the UNC5H-
CC 1 protein. The present sequence represents the human netrin binding

PR 10-JUN-2002; 2002US-0387535P.
PR 11-JUN-2002; 2002US-0387610P.
PR 11-JUN-2002; 2002US-0387625P.
PR 11-JUN-2002; 2002US-0387634P.
PR 11-JUN-2002; 2002US-0387668P.
PR 11-JUN-2002; 2002US-0387696P.
PR 11-JUN-2002; 2002US-0387702P.
PR 11-JUN-2002; 2002US-0387836P.
PR 11-JUN-2002; 2002US-0387859P.
PR 12-JUN-2002; 2002US-0387933P.
PR 12-JUN-2002; 2002US-0387934P.
PR 12-JUN-2002; 2002US-0387960P.
PR 12-JUN-2002; 2002US-0388022P.
PR 12-JUN-2002; 2002US-0388096P.
PR 13-JUN-2002; 2002US-0389123P.
PR 14-JUN-2002; 2002US-0389118P.
PR 14-JUN-2002; 2002US-0389120P.
PR 14-JUN-2002; 2002US-0389144P.
PR 14-JUN-2002; 2002US-0389146P.
PR 17-JUN-2002; 2002US-0389729P.
PR 17-JUN-2002; 2002US-0389742P.
PR 18-JUN-2002; 2002US-0389884P.
PR 19-JUN-2002; 2002US-0390006P.
PR 19-JUN-2002; 2002US-0390209P.
PR 21-JUN-2002; 2002US-0390763P.
PR 17-JUL-2002; 2002US-0396706P.
PR 06-AUG-2002; 2002US-0401628P.
PR 09-AUG-2002; 2002US-0402156P.
PR 09-AUG-2002; 2002US-0402256P.
PR 09-AUG-2002; 2002US-0402389P.
PR 12-AUG-2002; 2002US-0402786P.
PR 12-AUG-2002; 2002US-0402816P.
PR 12-AUG-2002; 2002US-0402821P.
PR 12-AUG-2002; 2002US-0402832P.
PR 13-AUG-2002; 2002US-0403448P.
PR 13-AUG-2002; 2002US-0403459P.
PR 13-AUG-2002; 2002US-0403531P.
PR 13-AUG-2002; 2002US-0403532P.
PR 13-AUG-2002; 2002US-0403563P.
PR 13-AUG-2002; 2002US-0406317P.
PR 15-AUG-2002; 2002US-0403617P.
PR 26-AUG-2002; 2002US-0406182P.
PR 26-AUG-2002; 2002US-0406355P.
PR 27-AUG-2002; 2002US-0406240P.
PR 12-SEP-2002; 2002US-0410084P.
PR 20-SEP-2002; 2002US-0412528P.
PR 23-SEP-2002; 2002US-0412731P.
PR 30-SEP-2002; 2002US-0414801P.
PR 30-SEP-2002; 2002US-0414839P.
PR 30-SEP-2002; 2002US-0414840P.
PR 30-SEP-2002; 2002US-0414954P.
PR 09-OCT-2002; 2002US-0417186P.
PR 09-OCT-2002; 2002US-0417406P.
PR 23-OCT-2002; 2002US-0420639P.
PR 28-OCT-2002; 2002US-0421156P.
PR 31-OCT-2002; 2002US-0422690P.
PR 01-NOV-2002; 2002US-0423130P.

PR 05-NOV-2002; 2002US-00423798.
PR 05-NOV-2002; 2002US-0423798P.
PR 12-NOV-2002; 2002US-0425453P.

XX

PA (CURA-) CURAGEN CORP.

XX

PI Alsobrook JP, Alvarez E, Anderson DW, Boldog FL, Casman SJ;
PI Catterton E, Chapoval A, Crabtree-Bokor JR, Edinger SR, Ellerman K;
PI Ettenberg S, Gangolli EA, Gerlach VL, Gorman L, Gunther E, Guo X;
PI Gusev VY, Herrmann JL, Ji W, Kekuda R, Li L, Liu X, Macdougall JR;
PI Maclachlan T, Malyankar UM, Mezick AJ, Millet I, Mishra VS;
PI Padigar M, Patturajan M, Pena CEA, Peyman JA, Raha D, Rastelli L;
PI Rieger DK, Rothenberg ME, Sciore P, Shenoy SG, Shinkets RA;
PI Smithson G, Spytek KA, Stone DJ, Vernet CAM, Voss EZ, Zhong M;
PI Zhong H;

XX

DR WPI; 2004-081935/08.

DR N-PSDB; ADH71617.

XX

PT New NOVX polypeptides and nucleic acid molecules useful for preventing or
PT treating NOVX-associated disorders, e.g. cancer, diabetes, infection or
PT obesity, and in chromosome mapping, tissue typing or pharmacogenomics.

XX

PS Example 21; SEQ ID NO 514; 1880pp; English.

XX

CC The invention relates to a novel isolated polypeptide (NOVX). A
CC polypeptide of the invention has cytostatic, immunomodulator,
CC neuroprotective, nootropic, anorectic, antidiabetic, antimicrobial, and
CC antilipaemic activity, and may have a use in gene therapy, and as a
CC vaccine. The polypeptides are encoded by NOVX polynucleotides comprising
CC any of the 303 fully defined nucleotide sequences given in the
CC specification. The polypeptide is useful in the manufacture of a
CC medicament for treating a syndrome associated with a human disease. The
CC polypeptide, polynucleotide and antibody are useful in diagnosing,
CC treating or preventing NOVX-associated disorders, e.g. cancer, cachexia,
CC Alzheimer's disease, Parkinson's disease, obesity, diabetes, infectious
CC diseases, metabolic syndrome X or dyslipidaemias. The nucleic acids are
CC further used as hybridisation probes, in chromosome mapping, tissue
CC typing, preventive medicine, and pharmacogenomics. The present sequence
CC represents a NOVX polypeptide of the invention.

XX

SQ Sequence 898 AA;

Query Match 100.0%; Score 559; DB 8; Length 898;
Best Local Similarity 100.0%; Pred. No. 3e-57;
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TSNMTYGTFFNLGGRLMIPNTGISLLIPDAIPRGKIYEIYLTLLHKPEDVRLPLAGCQTL 60
|
Db 495 TSNMTYGTFFNLGGRLMIPNTGISLLIPDAIPRGKIYEIYLTLLHKPEDVRLPLAGCQTL 554

Qy 61 LSPIVSCGPPGVLLTRPVILAMDHCGEPSWLSRLKKQSCEG 104
|
Db 555 LSPIVSCGPPGVLLTRPVILAMDHCGEPSWLSRLKKQSCEG 598

RESULT 10

ADH71626

ID ADH71626 standard; protein; 898 AA.

XX

AC ADH71626;

XX

DT 25-MAR-2004 (first entry)

XX

DE Human protein of the invention NOV21i SEQ ID NO:522.

XX

KW human; cytostatic; immunomodulator; neuroprotective; nootropic;
KW anorectic; antidiabetic; antimicrobial; antilipaemic; gene therapy;
KW vaccine; cancer; cachexia; Alzheimer's disease; Parkinson's disease;
KW obesity; diabetes; infectious disease; metabolic syndrome X;
KW dyslipidaemia.

XX

OS Homo sapiens.

XX

PN WO2003102155-A2.

XX

PD 11-DEC-2003.

XX

PF 03-JUN-2003; 2003WO-US017430.

XX

PR 03-JUN-2002; 2002US-0385120P.

PR 04-JUN-2002; 2002US-0385784P.

PR 05-JUN-2002; 2002US-0386041P.

PR 05-JUN-2002; 2002US-0386047P.

PR 06-JUN-2002; 2002US-0386376P.

PR 06-JUN-2002; 2002US-0386453P.

PR 06-JUN-2002; 2002US-0386864P.

PR 06-JUN-2002; 2002US-0387016P.

PR 07-JUN-2002; 2002US-0386796P.

PR 07-JUN-2002; 2002US-0386816P.

PR 07-JUN-2002; 2002US-0386931P.

PR 07-JUN-2002; 2002US-0386942P.

PR 07-JUN-2002; 2002US-0386971P.

PR 07-JUN-2002; 2002US-0387262P.

PR 08-JUN-2002; 2002US-0296960P.

PR 10-JUN-2002; 2002US-0387400P.

PR 10-JUN-2002; 2002US-0387535P.

PR 11-JUN-2002; 2002US-0387610P.

PR 11-JUN-2002; 2002US-0387625P.

PR 11-JUN-2002; 2002US-0387634P.

PR 11-JUN-2002; 2002US-0387668P.

PR 11-JUN-2002; 2002US-0387696P.

PR 11-JUN-2002; 2002US-0387702P.

PR 11-JUN-2002; 2002US-0387836P.

PR 11-JUN-2002; 2002US-0387859P.

PR 12-JUN-2002; 2002US-0387933P.

PR 12-JUN-2002; 2002US-0387934P.

PR 12-JUN-2002; 2002US-0387960P.

PR 12-JUN-2002; 2002US-0388022P.

PR 12-JUN-2002; 2002US-0388096P.

PR 13-JUN-2002; 2002US-0389123P.

PR 14-JUN-2002; 2002US-0389118P.

PR 14-JUN-2002; 2002US-0389120P.

PR 14-JUN-2002; 2002US-0389144P.

PR 14-JUN-2002; 2002US-0389146P.
PR 17-JUN-2002; 2002US-0389729P.
PR 17-JUN-2002; 2002US-0389742P.
PR 18-JUN-2002; 2002US-0389884P.
PR 19-JUN-2002; 2002US-0390006P.
PR 19-JUN-2002; 2002US-0390209P.
PR 21-JUN-2002; 2002US-0390763P.
PR 17-JUL-2002; 2002US-0396706P.
PR 06-AUG-2002; 2002US-0401628P.
PR 09-AUG-2002; 2002US-0402156P.
PR 09-AUG-2002; 2002US-0402256P.
PR 09-AUG-2002; 2002US-0402389P.
PR 12-AUG-2002; 2002US-0402786P.
PR 12-AUG-2002; 2002US-0402816P.
PR 12-AUG-2002; 2002US-0402821P.
PR 12-AUG-2002; 2002US-0402832P.
PR 13-AUG-2002; 2002US-0403448P.
PR 13-AUG-2002; 2002US-0403459P.
PR 13-AUG-2002; 2002US-0403531P.
PR 13-AUG-2002; 2002US-0403532P.
PR 13-AUG-2002; 2002US-0403563P.
PR 13-AUG-2002; 2002US-0406317P.
PR 15-AUG-2002; 2002US-0403617P.
PR 26-AUG-2002; 2002US-0406182P.
PR 26-AUG-2002; 2002US-0406355P.
PR 27-AUG-2002; 2002US-0406240P.
PR 12-SEP-2002; 2002US-0410084P.
PR 20-SEP-2002; 2002US-0412528P.
PR 23-SEP-2002; 2002US-0412731P.
PR 30-SEP-2002; 2002US-0414801P.
PR 30-SEP-2002; 2002US-0414839P.
PR 30-SEP-2002; 2002US-0414840P.
PR 30-SEP-2002; 2002US-0414954P.
PR 09-OCT-2002; 2002US-0417186P.
PR 09-OCT-2002; 2002US-0417406P.
PR 23-OCT-2002; 2002US-0420639P.
PR 28-OCT-2002; 2002US-0421156P.
PR 31-OCT-2002; 2002US-0422690P.
PR 01-NOV-2002; 2002US-0423130P.
PR 05-NOV-2002; 2002US-00423798.
PR 05-NOV-2002; 2002US-0423798P.
PR 12-NOV-2002; 2002US-0425453P.

XX

PA (CURA-) CURAGEN CORP.

XX

PI Alsobrook JP, Alvarez E, Anderson DW, Boldog FL, Casman SJ;
PI Catterton E, Chapoval A, Crabtree-Bokor JR, Edinger SR, Ellerman K;
PI Ettenberg S, Gangolli EA, Gerlach VL, Gorman L, Günther E, Guo X;
PI Gusev VY, Herrmann JL, Ji W, Kekuda R, Li L, Liu X, Macdougall JR;
PI Maclachlan T, Malyankar UM, Mezick AJ, Millet I, Mishra VS;
PI Padigar M, Patturajan M, Pena CEA, Peyman JA, Raha D, Rastelli L;
PI Rieger DK, Rothenberg ME, Sciore P, Shenoy SG, Shimkets RA;
PI Smithson G, Spytek KA, Stone DJ, Vernet CAM, Voss EZ, Zhong M;
PI Zhong H;

XX

DR WPI; 2004-081935/08.

DR N-PSDB; ADH71625.

PD 11-APR-2002.
 XX
 PF 04-OCT-2001; 2001WO-US031377.
 XX
 PR 04-OCT-2000; 2000US-0237862P.
 XX
 PA (CURA-) CURAGEN CORP.
 XX
 PI Herrmann JL, Rastelli L, Shimkets RA;
 XX
 DR WPI; 2002-340104/37.
 DR N-PSDB; ABK49422.
 XX
 PT Novel isolated NOVX polypeptide, and encoded polynucleotide, useful for
 PT treating cardiomyopathy, arteriosclerosis, and cancer.
 XX
 PS Claim 1; Page 9; 180pp; English.
 XX
 CC The present invention relates to a new NOVX polypeptide having a 900
 CC (NOV1), 4349 (NOV2), 940 (NOV3), 798 (NOV4), 865 (NOV5), or 331 (NOV6)
 CC residue amino acid sequence, as given in the specification. The novel
 CC polypeptide, and its encoding polynucleotide, are used to treat
 CC cardiomyopathy, atherosclerosis, cancer or a disease related to cell
 CC signal processing and metabolic pathway modulation, in a human. Detecting
 CC the polypeptide or polynucleotide is useful for identifying cancerous
 CC tissue. The antibody can be used to treat diabetes or cancer. The host
 CC cells can be used to produce non-human transgenic animals useful in drug
 CC screening. The present amino acid sequence is that of the human UNC5-like
 CC protein NOV1 of the invention. This sequence is encoded by the human UNC5
 CC -like NOV1 gene located on chromosome 13
 XX
 SQ Sequence 899 AA;

Query Match 100.0%; Score 559; DB 5; Length 899;
 Best Local Similarity 100.0%; Pred. No. 3e-57;
 Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TSNMTYGTFFNLGGRLMIPNTGISLLIPDAIPRGKIYEIYLT LHKPEDVRLPLAGCQTL 60
 ||||||||||||||||||||||||||||||||||||||||||||||||
 Db 495 TSNMTYGTFFNLGGRLMIPNTGISLLIPDAIPRGKIYEIYLT LHKPEDVRLPLAGCQTL 554

 Qy 61 LSPIVSCGPPGVLLTRPVILAMDHCGEPSDWSLRLKKQSCEG 104
 ||||||||||||||||||||||||||||||||||||||||||||||||
 Db 555 LSPIVSCGPPGVLLTRPVILAMDHCGEPSDWSLRLKKQSCEG 598

RESULT 12
 ADG42569

ID ADG42569 standard; protein; 899 AA.
 XX
 AC ADG42569;
 XX
 DT 26-FEB-2004 (first entry)
 XX
 DE Novel human NOV1.
 XX
 KW cytostatic; gene therapy; NOVX-agonist; NOVX-antagonist; pharmaceutical;

KW NOVX-associated disorder; cancer; human.
 XX
 OS Homo sapiens.
 XX
 PN US2003204052-A1.
 XX
 PD 30-OCT-2003.
 XX
 PF 04-OCT-2001; 2001US-00970944.
 XX
 PR 04-OCT-2000; 2000US-0237862P.
 XX
 PA (HERR/) HERRMANN J L.
 PA (RAST/) RASTELLI L.
 PA (SHIM/) SHIMKETS R A.
 XX
 PI Herrmann JL, Rastelli L, Shimkets RA;
 XX
 DR WPI; 2003-900673/82.
 DR N-PSDB; ADG42568.
 XX
 PT New NOVX gene or NOVX-specific antibody, useful for preparing a
 PT composition for treating or preventing a NOVX-associated disorder, e.g.,
 PT cancer.
 XX
 PS Claim 1; SEQ ID NO 2; 118pp; English.
 XX
 CC The invention describes a new isolated polypeptide comprising: a
 CC polypeptide or its mature form comprising a sequence not given in the
 CC specification; or a variant of (A), where one or more amino acid residues
 CC in the variant differs in no more than 15% from the amino acid sequence
 CC of the mature form. The pharmaceutical composition may be administered
 CC via oral, transdermal, rectal or parenteral route. The polypeptide,
 CC nucleic acid or antibody is useful for preparing a composition for
 CC treating or preventing a NOVX-associated disorder, e.g., cancer. This is
 CC the amino acid sequence of a human NOVX protein.
 XX
 SQ Sequence 899 AA;

Query Match 100.0%; Score 559; DB 7; Length 899;
 Best Local Similarity 100.0%; Pred. No. 3e-57;
 Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TSNMTYGTFFNFGGRLMIPNTGISLLIPDAIPRGKIYEIYLT LHKPEDVRLPLAGCQTL 60
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 495 TSNMTYGTFFNFGGRLMIPNTGISLLIPDAIPRGKIYEIYLT LHKPEDVRLPLAGCQTL 554
 Qy 61 LSPIVSCGPPGVLLTRPVILAMDHCGEPSDPSWSLRLKKQSCEG 104
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 555 LSPIVSCGPPGVLLTRPVILAMDHCGEPSDPSWSLRLKKQSCEG 598

RESULT 13
 ADH71636
 ID ADH71636 standard; protein; 899 AA.
 XX
 AC ADH71636;

XX
DT 25-MAR-2004 (first entry)
XX
DE Human protein of the invention NOV21n SEQ ID NO:532.
XX
KW human; cytostatic; immunomodulator; neuroprotective; nootropic;
KW anorectic; antidiabetic; antimicrobial; antilipaemic; gene therapy;
KW vaccine; cancer; cachexia; Alzheimer's disease; Parkinson's disease;
KW obesity; diabetes; infectious disease; metabolic syndrome X;
KW dyslipidaemia.
XX
OS Homo sapiens.
XX
PN WO2003102155-A2.
XX
PD 11-DEC-2003.
XX
PF 03-JUN-2003; 2003WO-US017430.
XX
PR 03-JUN-2002; 2002US-0385120P.
PR 04-JUN-2002; 2002US-0385784P.
PR 05-JUN-2002; 2002US-0386041P.
PR 05-JUN-2002; 2002US-0386047P.
PR 06-JUN-2002; 2002US-0386376P.
PR 06-JUN-2002; 2002US-0386453P.
PR 06-JUN-2002; 2002US-0386864P.
PR 06-JUN-2002; 2002US-0387016P.
PR 07-JUN-2002; 2002US-0386796P.
PR 07-JUN-2002; 2002US-0386816P.
PR 07-JUN-2002; 2002US-0386931P.
PR 07-JUN-2002; 2002US-0386942P.
PR 07-JUN-2002; 2002US-0386971P.
PR 07-JUN-2002; 2002US-0387262P.
PR 08-JUN-2002; 2002US-0296960P.
PR 10-JUN-2002; 2002US-0387400P.
PR 10-JUN-2002; 2002US-0387535P.
PR 11-JUN-2002; 2002US-0387610P.
PR 11-JUN-2002; 2002US-0387625P.
PR 11-JUN-2002; 2002US-0387634P.
PR 11-JUN-2002; 2002US-0387668P.
PR 11-JUN-2002; 2002US-0387696P.
PR 11-JUN-2002; 2002US-0387702P.
PR 11-JUN-2002; 2002US-0387836P.
PR 11-JUN-2002; 2002US-0387859P.
PR 12-JUN-2002; 2002US-0387933P.
PR 12-JUN-2002; 2002US-0387934P.
PR 12-JUN-2002; 2002US-0387960P.
PR 12-JUN-2002; 2002US-0388022P.
PR 12-JUN-2002; 2002US-0388096P.
PR 13-JUN-2002; 2002US-0389123P.
PR 14-JUN-2002; 2002US-0389118P.
PR 14-JUN-2002; 2002US-0389120P.
PR 14-JUN-2002; 2002US-0389144P.
PR 14-JUN-2002; 2002US-0389146P.
PR 17-JUN-2002; 2002US-0389729P.
PR 17-JUN-2002; 2002US-0389742P.
PR 18-JUN-2002; 2002US-0389884P.

PR 19-JUN-2002; 2002US-0390006P.
PR 19-JUN-2002; 2002US-0390209P.
PR 21-JUN-2002; 2002US-0390763P.
PR 17-JUL-2002; 2002US-0396706P.
PR 06-AUG-2002; 2002US-0401628P.
PR 09-AUG-2002; 2002US-0402156P.
PR 09-AUG-2002; 2002US-0402256P.
PR 09-AUG-2002; 2002US-0402389P.
PR 12-AUG-2002; 2002US-0402786P.
PR 12-AUG-2002; 2002US-0402816P.
PR 12-AUG-2002; 2002US-0402821P.
PR 12-AUG-2002; 2002US-0402832P.
PR 13-AUG-2002; 2002US-0403448P.
PR 13-AUG-2002; 2002US-0403459P.
PR 13-AUG-2002; 2002US-0403531P.
PR 13-AUG-2002; 2002US-0403532P.
PR 13-AUG-2002; 2002US-0403563P.
PR 13-AUG-2002; 2002US-0406317P.
PR 15-AUG-2002; 2002US-0403617P.
PR 26-AUG-2002; 2002US-0406182P.
PR 26-AUG-2002; 2002US-0406355P.
PR 27-AUG-2002; 2002US-0406240P.
PR 12-SEP-2002; 2002US-0410084P.
PR 20-SEP-2002; 2002US-0412528P.
PR 23-SEP-2002; 2002US-0412731P.
PR 30-SEP-2002; 2002US-0414801P.
PR 30-SEP-2002; 2002US-0414839P.
PR 30-SEP-2002; 2002US-0414840P.
PR 30-SEP-2002; 2002US-0414954P.
PR 09-OCT-2002; 2002US-0417186P.
PR 09-OCT-2002; 2002US-0417406P.
PR 23-OCT-2002; 2002US-0420639P.
PR 28-OCT-2002; 2002US-0421156P.
PR 31-OCT-2002; 2002US-0422690P.
PR 01-NOV-2002; 2002US-0423130P.
PR 05-NOV-2002; 2002US-00423798.
PR 05-NOV-2002; 2002US-0423798P.
PR 12-NOV-2002; 2002US-0425453P.

XX

PA (CURA-) CURAGEN CORP.

XX

PI Alsobrook JP, Alvarez E, Anderson DW, Boldog FL, Casman SJ;
PI Catterton E, Chapoval A, Crabtree-Bokor JR, Edinger SR, Ellerman K;
PI Ettenberg S, Gangolli EA, Gerlach VL, Gorman L, Gunther E, Guo X;
PI Gusev VY, Herrmann JL, Ji W, Kekuda R, Li L, Liu X, Macdougall JR;
PI Maclachlan T, Malyankar UM, Mezick AJ, Millet I, Mishra VS;
PI Padigar M, Patturajan M, Pena CEA, Peyman JA, Raha D, Rastelli L;
PI Rieger DK, Rothenberg ME, Sciore P, Shenoy SG, Shimkets RA;
PI Smithson G, Spytek KA, Stone DJ, Vernet CAM, Voss EZ, Zhong M;
PI Zhong H;

XX

DR WPI; 2004-081935/08.

DR N-PSDB; ADH71635.

XX

PT New NOVX polypeptides and nucleic acid molecules useful for preventing or
PT treating NOVX-associated disorders, e.g. cancer, diabetes, infection or
PT obesity, and in chromosome mapping, tissue typing or pharmacogenomics.

XX
 PS Example 21; SEQ ID NO 532; 1880pp; English.
 XX
 CC The invention relates to a novel isolated polypeptide (NOVX). A
 CC polypeptide of the invention has cytostatic, immunomodulator,
 CC neuroprotective, nootropic, anorectic, antidiabetic, antimicrobial, and
 CC antilipaemic activity, and may have a use in gene therapy, and as a
 CC vaccine. The polypeptides are encoded by NOVX polynucleotides comprising
 CC any of the 303 fully defined nucleotide sequences given in the
 CC specification. The polypeptide is useful in the manufacture of a
 CC medicament for treating a syndrome associated with a human disease. The
 CC polypeptide, polynucleotide and antibody are useful in diagnosing,
 CC treating or preventing NOVX-associated disorders, e.g. cancer, cachexia,
 CC Alzheimer's disease, Parkinson's disease, obesity, diabetes, infectious
 CC diseases, metabolic syndrome X or dyslipidaemias. The nucleic acids are
 CC further used as hybridisation probes, in chromosome mapping, tissue
 CC typing, preventive medicine, and pharmacogenomics. The present sequence
 CC represents a NOVX polypeptide of the invention.
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 SQ Sequence 899 AA;

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 Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 14

ADH71642

ID ADH71642 standard; protein; 899 AA.

XX

AC ADH71642;

XX

DT 25-MAR-2004 (first entry)

XX

DE Human protein of the invention NOV21q SEQ ID NO:538.

XX

KW human; cytostatic; immunomodulator; neuroprotective; nootropic;
 KW anorectic; antidiabetic; antimicrobial; antilipaemic; gene therapy;
 KW vaccine; cancer; cachexia; Alzheimer's disease; Parkinson's disease;
 KW obesity; diabetes; infectious disease; metabolic syndrome X;
 KW dyslipidaemia.

XX

OS Homo sapiens.

XX

PN WO2003102155-A2.

XX

PD 11-DEC-2003.

XX

PF 03-JUN-2003; 2003WO-US017430.

XX

PR 03-JUN-2002; 2002US-0385120P.
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PR 01-NOV-2002; 2002US-0423130P.
PR 05-NOV-2002; 2002US-00423798.
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PR 12-NOV-2002; 2002US-0425453P.

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PA (CURA-) CURAGEN CORP.

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PI Ettenberg S, Gangolli EA, Gerlach VL, Gorman L, Gunther E, Guo X;
PI Gusev VY, Herrmann JL, Ji W, Kekuda R, Li L, Liu X, Macdougall JR;
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PI Padigar M, Patturajan M, Pena CEA, Peyman JA, Raha D, Rastelli L;
PI Rieger DK, Rothenberg ME, Sciore P, Shenoy SG, Shimkets RA;
PI Smithson G, Spytek KA, Stone DJ, Vernet CAM, Voss EZ, Zhong M;
PI Zhong H;

XX

DR WPI; 2004-081935/08.

DR N-PSDB; ADH71641.

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PT New NOVX polypeptides and nucleic acid molecules useful for preventing or
PT treating NOVX-associated disorders, e.g. cancer, diabetes, infection or
PT obesity, and in chromosome mapping, tissue typing or pharmacogenomics.

XX

PS Example 21; SEQ ID NO 538; 1880pp; English.

XX

CC The invention relates to a novel isolated polypeptide (NOVX). A
CC polypeptide of the invention has cytostatic, immunomodulator,
CC neuroprotective, nootropic, anorectic, antidiabetic, antimicrobial, and
CC antilipaemic activity, and may have a use in gene therapy, and as a
CC vaccine. The polypeptides are encoded by NOVX polynucleotides comprising
CC any of the 303 fully defined nucleotide sequences given in the
CC specification. The polypeptide is useful in the manufacture of a
CC medicament for treating a syndrome associated with a human disease. The
CC polypeptide, polynucleotide and antibody are useful in diagnosing,
CC treating or preventing NOVX-associated disorders, e.g. cancer, cachexia,
CC Alzheimer's disease, Parkinson's disease, obesity, diabetes, infectious
CC diseases, metabolic syndrome X or dyslipidaemias. The nucleic acids are
CC further used as hybridisation probes, in chromosome mapping, tissue
CC typing, preventive medicine, and pharmacogenomics. The present sequence
CC represents a NOVX polypeptide of the invention.

XX
SQ Sequence 899 AA;

Query Match 100.0%; Score 559; DB 8; Length 899;
Best Local Similarity 100.0%; Pred. No. 3e-57;
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TSNMTYGTFFNLGGRLMIPNTGISLLIPDAIPRGKIYEIYLT LHKPEDVRLPLAGCQTL 60
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RESULT 15

ADH71648

ID ADH71648 standard; protein; 899 AA.

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AC ADH71648;

XX

DT 25-MAR-2004 (first entry)

XX

DE Human protein of the invention NOV21t SEQ ID NO:544.

XX

KW human; cytostatic; immunomodulator; neuroprotective; nootropic;
KW anorectic; antidiabetic; antimicrobial; antilipaemic; gene therapy;
KW vaccine; cancer; cachexia; Alzheimer's disease; Parkinson's disease;
KW obesity; diabetes; infectious disease; metabolic syndrome X;
KW dyslipidaemia.

XX

OS Homo sapiens.

XX

PN WO2003102155-A2.

XX

PD 11-DEC-2003.

XX

PF 03-JUN-2003; 2003WO-US017430.

XX

PR 03-JUN-2002; 2002US-0385120P.

PR 04-JUN-2002; 2002US-0385784P.

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PR 06-JUN-2002; 2002US-0386376P.

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PR 01-NOV-2002; 2002US-0423130P.
PR 05-NOV-2002; 2002US-00423798.

GenCore version 5.1.6
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	553	98.9	898	2	US-08-808-982-5	Sequence 5, Appli
4	553	98.9	898	3	US-09-306-902A-5	Sequence 5, Appli
5	337	60.3	769	4	US-09-949-016-10665	Sequence 10665, A
6	277	49.6	943	2	US-08-808-982-7	Sequence 7, Appli
7	277	49.6	943	3	US-09-306-902A-7	Sequence 7, Appli
8	243.5	43.6	655	4	US-09-969-532-32	Sequence 32, Appl
9	243.5	43.6	666	4	US-09-969-532-30	Sequence 30, Appl
10	243.5	43.6	669	4	US-09-969-532-28	Sequence 28, Appl
11	243.5	43.6	680	4	US-09-969-532-26	Sequence 26, Appl

12	243.5	43.6	886	4	US-09-969-532-16	Sequence 16, Appl
13	243.5	43.6	897	4	US-09-969-532-14	Sequence 14, Appl
14	243.5	43.6	900	4	US-09-969-532-12	Sequence 12, Appl
15	243.5	43.6	911	4	US-09-969-532-10	Sequence 10, Appl
16	163.5	29.2	1736	4	US-09-919-497-98	Sequence 98, Appl
17	163.5	29.2	1771	4	US-09-949-016-9470	Sequence 9470, Ap
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ALIGNMENTS

RESULT 1

US-08-808-982-6

; Sequence 6, Application US/08808982

; Patent No. 5939271

; GENERAL INFORMATION:

; APPLICANT: Tessier-Lavigne, Marc

; APPLICANT: Leonardo, E. David

; APPLICANT: Hink, Lindsay

; APPLICANT: Masu, Masayuki

; APPLICANT: Kazuko, Keino-Masu

; TITLE OF INVENTION: Netrin Receptors

; NUMBER OF SEQUENCES: 8

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP

; STREET: 268 BUSH STREET, SUITE 3200

; CITY: SAN FRANCISCO

; STATE: CALIFORNIA

; COUNTRY: USA

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; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/808,982
; FILING DATE:
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: OSMAN, RICHARD A
; REGISTRATION NUMBER: 36,627
; REFERENCE/DOCKET NUMBER: UC96-217
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 343-4341
; TELEFAX: (415) 343-4342
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 557 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: not relevant
; MOLECULE TYPE: peptide
US-08-808-982-6

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Query Match          98.9%; Score 553; DB 2; Length 557;
Best Local Similarity 99.0%; Pred. No. 1.2e-60;
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Qy      1 TSNMTYGTFFNFLGGRLMIPNTGISLLIPPDAIPRGKIYEIYLT LHKPEDVRLPLAGCQTL 60
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RESULT 2

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; Sequence 6, Application US/09306902A

; Patent No. 6277585

; GENERAL INFORMATION:

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; APPLICANT: Tessier-Lavigne, Marc
;           Leonardo, E. David
;           Hink, Lindsay
;           Masu, Masayuki
;           Kazuko, Keino-Masu

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; TITLE OF INVENTION: Netrin Receptors

; NUMBER OF SEQUENCES: 9

; CORRESPONDENCE ADDRESS:

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; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
; STREET: 268 BUSH STREET, SUITE 3200
; CITY: SAN FRANCISCO
; STATE: CALIFORNIA
; COUNTRY: USA

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;           ZIP: 94104
;   COMPUTER READABLE FORM:
;           MEDIUM TYPE: Floppy disk
;           COMPUTER: IBM PC compatible
;           OPERATING SYSTEM: PC-DOS/MS-DOS
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;   CURRENT APPLICATION DATA:
;           APPLICATION NUMBER: US/09/306,902A
;           FILING DATE: 07-May-1999
;           CLASSIFICATION: <Unknown>
;   ATTORNEY/AGENT INFORMATION:
;           NAME: OSMAN, RICHARD A
;           REGISTRATION NUMBER: 36,627
;           REFERENCE/DOCKET NUMBER: UC96-217
;   TELECOMMUNICATION INFORMATION:
;           TELEPHONE: (415) 343-4341
;           TELEFAX: (415) 343-4342
;   INFORMATION FOR SEQ ID NO: 6:
;       SEQUENCE CHARACTERISTICS:
;           LENGTH: 557 amino acids
;           TYPE: amino acid
;           STRANDEDNESS: not relevant
;           TOPOLOGY: not relevant
;       MOLECULE TYPE: peptide
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Query Match      98.9%; Score 553; DB 3; Length 557;
Best Local Similarity 99.0%; Pred. No. 1.2e-60;
Matches 103; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy      1 TSNMTYGTFTNFLGGRLMIPNTGISLLIPPDAIPRGKIYEIYLT LHKPEDVRLPLAGCQTL 60
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RESULT 3

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; Sequence 5, Application US/08808982
; Patent No. 5939271
;   GENERAL INFORMATION:
;       APPLICANT: Tessier-Lavigne, Marc
;       APPLICANT: Leonardo, E. David
;       APPLICANT: Hink, Lindsay
;       APPLICANT: Masu, Masayuki
;       APPLICANT: Kazuko, Keino-Masu
;       TITLE OF INVENTION: Netrin Receptors
;       NUMBER OF SEQUENCES: 8
;       CORRESPONDENCE ADDRESS:
;           ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
;           STREET: 268 BUSH STREET, SUITE 3200
;           CITY: SAN FRANCISCO
;           STATE: CALIFORNIA

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;          COUNTRY: USA
;          ZIP: 94104
;    COMPUTER READABLE FORM:
;          MEDIUM TYPE: Floppy disk
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;          OPERATING SYSTEM: PC-DOS/MS-DOS
;          SOFTWARE: PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;          APPLICATION NUMBER: US/09/306,902A
;          FILING DATE: 07-May-1999
;          CLASSIFICATION: <Unknown>
;    ATTORNEY/AGENT INFORMATION:
;          NAME: OSMAN, RICHARD A
;          REGISTRATION NUMBER: 36,627
;          REFERENCE/DOCKET NUMBER: UC96-217
;    TELECOMMUNICATION INFORMATION:
;          TELEPHONE: (415) 343-4341
;          TELEFAX: (415) 343-4342
;    INFORMATION FOR SEQ ID NO: 5:
;          SEQUENCE CHARACTERISTICS:
;            LENGTH: 898 amino acids
;            TYPE: amino acid
;            STRANDEDNESS: not relevant
;            TOPOLOGY: not relevant
;          MOLECULE TYPE: peptide
;          SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-09-306-902A-5

```

```

Query Match          98.9%;  Score 553;  DB 3;  Length 898;
Best Local Similarity 98.1%;  Pred. No. 2.2e-60;
Matches 102;  Conservative 1;  Mismatches 1;  Indels 0;  Gaps 0;

```

```

Qy      1 TSNMTYGTFFNFGGRLMIPNTGISLLIPPDAIPRGKIYEIYLT LHKPEDVRLPLAGCQTL 60
      ||| |||||||||||||||||||||||||||||||||||||||||
Db      495 TSNMAYGTFFNFGGRLMIPNTGISLLIPPDAIPRGKIYEIYLT LHKPEDVRLPLAGCQTL 554

Qy      61 LSPIVSCGPPGVLLTRPVILAMDHCGEPSDPSWSLRLKKQSCEG 104
      |||:|||||||||||||||||||||||||||||||||||
Db      555 LSPVVSCGPPGVLLTRPVILAMDHCGEPSDPSWSLRLKKQSCEG 598

```

```

RESULT 5
US-09-949-016-10665
; Sequence 10665, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;   APPLICANT: VENTER, J. Craig et al.
;   TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;   TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES
THEREOF
;   FILE REFERENCE: CL001307
;   CURRENT APPLICATION NUMBER: US/09/949,016
;   CURRENT FILING DATE: 2000-04-14
;   PRIOR APPLICATION NUMBER: 60/241,755
;   PRIOR FILING DATE: 2000-10-20
;   PRIOR APPLICATION NUMBER: 60/237,768
;   PRIOR FILING DATE: 2000-10-03

```

; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 10665
; LENGTH: 769
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-10665

Query Match 60.3%; Score 337; DB 4; Length 769;
Best Local Similarity 55.6%; Pred. No. 2.1e-33;
Matches 55; Conservative 24; Mismatches 20; Indels 0; Gaps 0;

Qy 6 YGTFNFLGGRLMIPNTGISLLIPDAIPRGKIYEIYLT LHKPEDVRLPLAGCQTLLSPIV 65
:|:| | | | :|:|:|:|:| | | :|:|:|:|:|:| | :| | : | | | :|:
Db 371 FGSFNSLGGHLIVPNSGVSLIPAGAI PQGRVYEMYVTVHRKETMRPPMDDSQTLLTPVV 430

Qy 66 SCGPPGVLLTRPVILAMDHCGEPSDWSLRLKKQSCEG 104
| | | | | | | | | | :| | | :|: | : | | :|:
Db 431 SCGPPGALLTRPVVLTMHHCADPNTEDWKILLKNQAAQG 469

RESULT 6

US-08-808-982-7

; Sequence 7, Application US/08808982
; Patent No. 5939271
; GENERAL INFORMATION:
; APPLICANT: Tessier-Lavigne, Marc
; APPLICANT: Leonardo, E. David
; APPLICANT: Hink, Lindsay
; APPLICANT: Masu, Masayuki
; APPLICANT: Kazuko, Keino-Masu
; TITLE OF INVENTION: Netrin Receptors
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
; STREET: 268 BUSH STREET, SUITE 3200
; CITY: SAN FRANCISCO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/808,982
; FILING DATE:
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: OSMAN, RICHARD A
; REGISTRATION NUMBER: 36,627
; REFERENCE/DOCKET NUMBER: UC96-217
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 343-4341

; TELEFAX: (415) 343-4342
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 943 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: not relevant
; MOLECULE TYPE: peptide
US-08-808-982-7

Query Match 49.6%; Score 277; DB 2; Length 943;
Best Local Similarity 52.9%; Pred. No. 9.1e-26;
Matches 55; Conservative 17; Mismatches 30; Indels 2; Gaps 2;

Qy 2 SNMTYGTFFNFLGGRLMIPNTGISLLIPDAIPRGKIYEIYLT LHKPEDVRLPLA-GCQTL 60
|: ||| |||| || ||:|||| | ||:| | |:| | :| | ||: | ||:
Db 540 SSSVSGTFGCLGGRLTIPGTGVSLLPNGAIPQGKFYDLYLRINKTEST-LPLSEGSQTV 598

Qy 61 LSPIVSCGPPGVLLTRPVILAMDHCGEPSDPSWSLRLKKQSCEG 104
||| |:| | |:| | ||:| : || | | :|| |: :|
Db 599 LSPSVTCGPTGLLLCRPVVLTVPHCAEVIAGDWIFQLKTOAHQG 642

RESULT 7

US-09-306-902A-7

; Sequence 7, Application US/09306902A
; Patent No. 6277585
; GENERAL INFORMATION:
; APPLICANT: Tessier-Lavigne, Marc
; Leonardo, E. David
; Hink, Lindsay
; Masu, Masayuki
; Kazuko, Keino-Masu
; TITLE OF INVENTION: Netrin Receptors
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
; STREET: 268 BUSH STREET, SUITE 3200
; CITY: SAN FRANCISCO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/306,902A
; FILING DATE: 07-May-1999
; CLASSIFICATION: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: OSMAN, RICHARD A
; REGISTRATION NUMBER: 36,627
; REFERENCE/DOCKET NUMBER: UC96-217
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 343-4341

; TELEFAX: (415) 343-4342
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 943 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: not relevant
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 7:
US-09-306-902A-7

Query Match 49.6%; Score 277; DB 3; Length 943;
Best Local Similarity 52.9%; Pred. No. 9.1e-26;
Matches 55; Conservative 17; Mismatches 30; Indels 2; Gaps 2;

Qy 2 SNMTYGTFFNGLGGRMLIPNTGISLLIPPDAPRGKIYEIYLTLLHKPEDVRLPLA-GCQTL 60
|: ||| |||| || ||:||||: |||:| |:| | :| | ||: | ||:
Db 540 SSSVSGTFGCLGGRLTIPGTGVSLLPNGAIPQGKFYDLYLRINKTEST-LPLSEGSQTV 598

Qy 61 LSPIVSCGPPGVLLTRPVILAMDHCGEPSDPSWSLRLKKQSCEG 104
||| |:||| |:| |||:| : || | | :|| |: :|
Db 599 LSPSVTCGPTGLLLCRPVVLTVPHCAEVIAGDWIFQLKTQAHQG 642

RESULT 8

US-09-969-532-32
; Sequence 32, Application US/09969532
; Patent No. 6777232
; GENERAL INFORMATION:
; APPLICANT: Walke, D. Wade
; APPLICANT: Scoville, John
; TITLE OF INVENTION: No. 6777232el Human Membrane Proteins and Polynucleotides
Encoding the Same
; FILE REFERENCE: LEX-0244-USA
; CURRENT APPLICATION NUMBER: US/09/969,532
; CURRENT FILING DATE: 2001-10-02
; PRIOR APPLICATION NUMBER: US 60/237,280
; PRIOR FILING DATE: 2000-10-02
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 32
; LENGTH: 655
; TYPE: PRT
; ORGANISM: homo sapiens
US-09-969-532-32

Query Match 43.6%; Score 243.5; DB 4; Length 655;
Best Local Similarity 45.2%; Pred. No. 8.9e-22;
Matches 47; Conservative 22; Mismatches 34; Indels 1; Gaps 1;

Qy 1 TSNMTYGTFFNGLGGRMLIPNTGISLLIPPDAPRGKIYEIYLTLLHKPEDVRLPLAGCQTL 60
| | | | ||||:||||:|||| ||| :|||::: | | | : |
Db 242 TELRTTGVFHGLGGRLVMPNTGVSLIPHGAIPEENSWEIYMSINQGEP-SLQSDGSEVL 300

Qy 61 LSPIVSCGPPGVLLTRPVILAMDHCGEPSDPSWSLRLKKQSCEG 104
||| |:||| ::| | | : || : | : |:| |||: :|
Db 301 LSPEVTCGPPDMIVTTTPFALTIPHCADVSSEHWNHLLKKRTQQG 344

```

US-09-969-532-30
; Sequence 30, Application US/09969532
; Patent No. 6777232
; GENERAL INFORMATION:
; APPLICANT: Walke, D. Wade
; APPLICANT: Scoville, John
; TITLE OF INVENTION: No. 6777232e1 Human Membrane Proteins and Polynucleotides
Encoding the Same
; FILE REFERENCE: LEX-0244-USA
; CURRENT APPLICATION NUMBER: US/09/969,532
; CURRENT FILING DATE: 2001-10-02
; PRIOR APPLICATION NUMBER: US 60/237,280
; PRIOR FILING DATE: 2000-10-02
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 30
; LENGTH: 666
; TYPE: PRT
; ORGANISM: homo sapiens
US-09-969-532-30

```

Query Match 43.6%; Score 243.5; DB 4; Length 666;
Best Local Similarity 45.2%; Pred. No. 9.1e-22;
Matches 47; Conservative 22; Mismatches 34; Indels 1; Gaps 1;

Qy	1	TSNMTYGT	FNFLGGRL	MIPNTG	ISLLIP	PD	AI	PRGKI	YEI	YLT	TLHK	PEDV	RLPL	AGC	QTL	60
Db	253	TELRTT	GVFGHL	GGRLV	MPNTG	VSL	LIP	PHGAI	PEEN	SWEI	YMSI	NQGE	P-SL	QSDG	SEVL	311
Qy	61	LSPIV	SCGPP	GVLL	TRPV	ILAM	DH	CGEP	SPDS	WSL	RLK	Q	SC	EG	104	
Db	312	LSPEV	TCGPP	DMIV	TTPF	ALT	IPHC	ADVS	SEH	WNI	HLK	R	TOO	G	355	

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US-09-969-532-28
; Sequence 28, Application US/09969532
; Patent No. 6777232
; GENERAL INFORMATION:
; APPLICANT: Walke, D. Wade
; APPLICANT: Scoville, John
; TITLE OF INVENTION: No. 6777232el Human Membrane Proteins and Polynucleotides
Encoding the Same
; FILE REFERENCE: LEX-0244-USA
; CURRENT APPLICATION NUMBER: US/09/969,532
; CURRENT FILING DATE: 2001-10-02
; PRIOR APPLICATION NUMBER: US 60/237,280
; PRIOR FILING DATE: 2000-10-02
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 28
; LENGTH: 669
; TYPE: PRT
; ORGANISM: homo sapiens

```

US-09-969-532-28

Query Match 43.6%; Score 243.5; DB 4; Length 669;
Best Local Similarity 45.2%; Pred. No. 9.2e-22;
Matches 47; Conservative 22; Mismatches 34; Indels 1; Gaps 1;

Qy 1 TSNMTYGTFFNLGGRLMIPNTGISLLIPPDAIPRGKIYEIYLT LHKPEDVRLPLAGCQTL 60
| | | | | : : : : : | | | : |
Db 256 TELRTTGVFGHLGGRLVMPNTGVSLIPHGAIPEENSWEIYMSINQGEP-SLQSDGSEVL 314

Qy 61 LSPIVSCGPPGVLLTRPVILAMDHCGEPSDPSWRLKQSCGE 104
| | | : : : : : | | : | : | : : : : :
Db 315 LSPEVTCGPPDMIVTTPFALTIPHCADVSSEHWNHLKRTQQG 358

RESULT 11

US-09-969-532-26

; Sequence 26, Application US/09969532
; Patent No. 6777232
; GENERAL INFORMATION:
; APPLICANT: Walke, D. Wade
; APPLICANT: Scoville, John
; TITLE OF INVENTION: No. 6777232el Human Membrane Proteins and Polynucleotides
Encoding the Same
; FILE REFERENCE: LEX-0244-USA
; CURRENT APPLICATION NUMBER: US/09/969,532
; CURRENT FILING DATE: 2001-10-02
; PRIOR APPLICATION NUMBER: US 60/237,280
; PRIOR FILING DATE: 2000-10-02
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 26
; LENGTH: 680
; TYPE: PRT
; ORGANISM: homo sapiens
US-09-969-532-26

Query Match 43.6%; Score 243.5; DB 4; Length 680;
Best Local Similarity 45.2%; Pred. No. 9.4e-22;
Matches 47; Conservative 22; Mismatches 34; Indels 1; Gaps 1;

Qy 1 TSNMTYGTFFNLGGRLMIPNTGISLLIPPDAIPRGKIYEIYLT LHKPEDVRLPLAGCQTL 60
| | | | | : : : : : | | | : |
Db 267 TELRTTGVFGHLGGRLVMPNTGVSLIPHGAIPEENSWEIYMSINQGEP-SLQSDGSEVL 325

Qy 61 LSPIVSCGPPGVLLTRPVILAMDHCGEPSDPSWRLKQSCGE 104
| | | : : : : : | | : | : | : : : : :
Db 326 LSPEVTCGPPDMIVTTPFALTIPHCADVSSEHWNHLKRTQQG 369

RESULT 12.

US-09-969-532-16

; Sequence 16, Application US/09969532
; Patent No. 6777232
; GENERAL INFORMATION:
; APPLICANT: Walke, D. Wade
; APPLICANT: Scoville, John

```
; TITLE OF INVENTION: No. 6777232e1 Human Membrane Proteins and Polynucleotides
Encoding the Same
; FILE REFERENCE: LEX-0244-USA
; CURRENT APPLICATION NUMBER: US/09/969,532
; CURRENT FILING DATE: 2001-10-02
; PRIOR APPLICATION NUMBER: US 60/237,280
; PRIOR FILING DATE: 2000-10-02
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 16
; LENGTH: 886
; TYPE: PRT
; ORGANISM: homo sapiens
US-09-969-532-16
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```
Query Match          43.6%; Score 243.5; DB 4; Length 886;
Best Local Similarity 45.2%; Pred. No. 1.3e-21;
Matches 47; Conservative 22; Mismatches 34; Indels 1; Gaps 1;
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```
Qy      1 TSNMTYGTFFNLGGRLMIPNTGISLLIPPDPAIPRGKIYEIYLTLLHKPEDVRLPLAGCQTL 60
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      473 TELRTTGVFGHLGGRLVMPNTGVSLIPHGAIPEENSWEIYMSINQGEP-SLQSDGSEVL 531

Qy      61 LSPIVSCGPPGVLLTRPVILAMDHCGEPSDWSLRLKKQSCGE 104
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      532 LSPEVTCGPPDMIVTTTPFALTIPHCADVSSEHWNHLLKKRTQQG 575
```

RESULT 13

```
US-09-969-532-14
; Sequence 14, Application US/09969532
; Patent No. 6777232
; GENERAL INFORMATION:
; APPLICANT: Walke, D. Wade
; APPLICANT: Scoville, John
; TITLE OF INVENTION: No. 6777232e1 Human Membrane Proteins and Polynucleotides
Encoding the Same
; FILE REFERENCE: LEX-0244-USA
; CURRENT APPLICATION NUMBER: US/09/969,532
; CURRENT FILING DATE: 2001-10-02
; PRIOR APPLICATION NUMBER: US 60/237,280
; PRIOR FILING DATE: 2000-10-02
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 14
; LENGTH: 897
; TYPE: PRT
; ORGANISM: homo sapiens
US-09-969-532-14
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```
Query Match          43.6%; Score 243.5; DB 4; Length 897;
Best Local Similarity 45.2%; Pred. No. 1.3e-21;
Matches 47; Conservative 22; Mismatches 34; Indels 1; Gaps 1;
```

```
Qy      1 TSNMTYGTFFNLGGRLMIPNTGISLLIPPDPAIPRGKIYEIYLTLLHKPEDVRLPLAGCQTL 60
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      484 TELRTTGVFGHLGGRLVMPNTGVSLIPHGAIPEENSWEIYMSINQGEP-SLQSDGSEVL 542
```

Qy 61 LSPIVSCGPPGVLLTRPVILAMDHCGEPSPDSWSLRLKKQSCEG 104
 ||| |:|||| ::| | | : || : | : |:: |||:: :|
 Db 543 LSPEVTCGPPDMIVTTTPFALTIPHCADVSSEHWNHLLKKRTQQG 586

RESULT 14

US-09-969-532-12

; Sequence 12, Application US/09969532
 ; Patent No. 6777232
 ; GENERAL INFORMATION:
 ; APPLICANT: Walke, D. Wade
 ; APPLICANT: Scoville, John
 ; TITLE OF INVENTION: No. 6777232el Human Membrane Proteins and Polynucleotides
 Encoding the Same
 ; FILE REFERENCE: LEX-0244-USA
 ; CURRENT APPLICATION NUMBER: US/09/969,532
 ; CURRENT FILING DATE: 2001-10-02
 ; PRIOR APPLICATION NUMBER: US 60/237,280
 ; PRIOR FILING DATE: 2000-10-02
 ; NUMBER OF SEQ ID NOS: 33
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO 12
 ; LENGTH: 900
 ; TYPE: PRT
 ; ORGANISM: homo sapiens
 US-09-969-532-12

Query Match 43.6%; Score 243.5; DB 4; Length 900;
 Best Local Similarity 45.2%; Pred. No. 1.4e-21;
 Matches 47; Conservative 22; Mismatches 34; Indels 1; Gaps 1;

Qy 1 TSNMTYGTGNFLGGRLMIPNTGISLLIPDAIPRGKIYEIYLTLLHKPEDVRLPLAGCQTL 60
 | | | | ||||::|||:|||| ||| :|||::: | | | : |
 Db 487 TELRTTGVFGHLGGRLVMPNTGVSLIPHGAIPEENSWEIYMSINQGEPSLQSDGSEVL 545

Qy 61 LSPIVSCGPPGVLLTRPVILAMDHCGEPSPDSWSLRLKKQSCEG 104
 ||| |:|||| ::| | | : || : | : |:: |||:: :|
 Db 546 LSPEVTCGPPDMIVTTTPFALTIPHCADVSSEHWNHLLKKRTQQG 589

RESULT 15

US-09-969-532-10

; Sequence 10, Application US/09969532
 ; Patent No. 6777232
 ; GENERAL INFORMATION:
 ; APPLICANT: Walke, D. Wade
 ; APPLICANT: Scoville, John
 ; TITLE OF INVENTION: No. 6777232el Human Membrane Proteins and Polynucleotides
 Encoding the Same
 ; FILE REFERENCE: LEX-0244-USA
 ; CURRENT APPLICATION NUMBER: US/09/969,532
 ; CURRENT FILING DATE: 2001-10-02
 ; PRIOR APPLICATION NUMBER: US 60/237,280
 ; PRIOR FILING DATE: 2000-10-02
 ; NUMBER OF SEQ ID NOS: 33
 ; SOFTWARE: FastSEQ for Windows Version 4.0

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; SEQ ID NO 10
;   LENGTH: 911
;   TYPE: PRT
;   ORGANISM: homo sapiens
US-09-969-532-10
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Query Match 43.6%; Score 243.5; DB 4; Length 911;
Best Local Similarity 45.2%; Pred. No. 1.4e-21;
Matches 47; Conservative 22; Mismatches 34; Indels 1; Gaps 1;

Qy 1 TSNM TYGT FNFLGGRLMIPNTGISLLIPDAIPRGKIYEIYLT LHKPEDVRLPLAGCQTL 60
| | | | | | | | : | | | : | | | | | : | | | : |
Db 498 TELRTTGVFGHLGGRLVMPNTGVSL LIPHGAIP EENSWEIYMSINQGE P-SLQSDGSEVL 556

Qy 61 LSPIVSCGPPGVLLTRPVILAMDHCGEPSDWSLRLKKQSCGE 104
||| |:|||| :::| | : || : | : :: |||:: :|

Db 557 LSPEVTCGPPDMIVTTTPFALTIPHCADVSSEHWNHLLKKRTQOG 600

Search completed: March 1, 2005, 09:05:53
Job time : 7.2315 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: March 1, 2005, 08:46:18 ; Search time 4.05992 Seconds
(without alignments)
2464.715 Million cell updates/sec

Title: US-10-624-932-2_COPY_495_598
Perfect score: 559
Sequence: 1 TSNMTYGTFTNGLGRLMIPN.....CGEPSPDSWSLRLKKQSCEG 104

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query		DB	ID	Description
		Match	Length			
1	163.5	29.2	1736	2	A47747	tight junction pro
2	162.5	29.1	1745	2	A46431	tight junction-ass
3	96	17.2	919	2	T32541	unc-5 protein - Ca
4	96	17.2	947	1	B44294	unc-5 protein, lon
5	76	13.6	346	2	S21265	acetylserotonin O-
6	73	13.1	1848	2	S37771	ankyrin, erythrocy
7	73	13.1	1862	2	I49502	ankyrin - mouse
8	72	12.9	1856	2	B35049	ankyrin 1, erythro
9	72	12.9	1880	2	A35049	ankyrin 1, erythro
10	72	12.9	1881	1	SJHUK	ankyrin 1, erythro
11	70	12.5	384	2	S73122	carbamoyl phosphat
12	69.5	12.4	369	2	D72240	tRNA guanine trans
13	69	12.3	345	2	I48780	Stral/Eplg2 protei

14	69	12.3	345	2	I58406	LERK-2 - rat
15	68	12.2	346	2	S46993	elk ligand - human
16	68	12.2	388	1	VCVGAC	coat protein - art
17	68	12.2	803	2	S76106	hypothetical prote
18	68	12.2	999	2	AG2413	hypothetical prote
19	66.5	11.9	285	2	B83883	sugar transport sy
20	66.5	11.9	544	2	C95854	probable trehalose
21	66	11.8	201	2	D82590	hypothetical prote
22	66	11.8	467	2	A60667	cysteine proteinas
23	65.5	11.7	217	2	T47175	hypothetical prote
24	65.5	11.7	235	2	G72484	hypothetical prote
25	65.5	11.7	411	2	A55610	corticotropin-rele
26	65	11.6	388	2	S24926	coat protein, 41K
27	64.5	11.5	467	2	A45629	cysteine proteinas
28	64	11.4	579	2	G75142	abc transporter, A
29	63.5	11.4	256	2	S74928	hypothetical prote
30	63.5	11.4	400	2	D83892	transcription regu
31	62.5	11.2	236	2	T40833	haloacid dehalogen
32	62.5	11.2	255	2	AD1946	hypothetical prote
33	62.5	11.2	260	2	G70568	hypothetical prote
34	62.5	11.2	363	2	B97199	uncharacterized co
35	62.5	11.2	498	1	VHIVA6	nucleoprotein - in
36	62	11.1	253	2	G72598	probable ABC trans
37	62	11.1	270	2	B83387	hypothetical prote
38	61.5	11.0	170	2	AI3322	hypothetical prote
39	61.5	11.0	434	1	DEEBHT	histidinol dehydro
40	61.5	11.0	445	2	D81716	hypothetical prote
41	61.5	11.0	710	2	D72091	type III secretion
42	61.5	11.0	710	2	C86531	low calcium respon
43	61.5	11.0	1022	2	T49683	probable oxoglutar
44	61.5	11.0	1396	2	T10627	hypothetical prote
45	61	10.9	99	2	S42360	capsicein - Phytop

ALIGNMENTS

RESULT 1

A47747

tight junction protein ZO-1 - human

C;Species: Homo sapiens (man)

C;Date: 02-Jun-1994 #sequence_revision 02-Jun-1994 #text_change 09-Jul-2004

C;Accession: A47747

R;Willott, E.; Balda, M.S.; Fanning, A.S.; Jameson, B.; Van Itallie, C.; Anderson, J.M.

Proc. Natl. Acad. Sci. U.S.A. 90, 7834-7838, 1993

A;Title: The tight junction protein ZO-1 is homologous to the Drosophila discs-large tumor suppressor protein of septate junctions.

A;Reference number: A47747; MUID:93361541; PMID:8395056

A;Accession: A47747

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-1736 <WIL>

A;Cross-references: UNIPROT:Q07157; GB:L14837; NID:g292937; PIDN:AAA02891.1; PID:g292938

C;Keywords: alternative splicing; membrane protein; phosphoprotein

F;15-94/Domain: GLGF domain homology <GLG1>

F;181-248/Domain: GLGF domain homology <GLG2>
F;416-486/Domain: GLGF domain homology <GLG3>
F;633-782/Domain: guanylate kinase homology <GKI>

Query Match 29.2%; Score 163.5; DB 2; Length 1736;
Best Local Similarity 41.6%; Pred. No. 3.6e-09;
Matches 37; Conservative 12; Mismatches 35; Indels 5; Gaps 2;

```
Qy      7 GTFNFLGGRLMIPNTGISLLIPPDAIPRGKIYEIYLT LHKPEDVRLPL--AGCQTLLSPI 64
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      1626 GIFNSNGGVLSIETGVSIIPQGAIPGVEQEYFKVCRDNSILPPLDKEKGETLLSPL 1685

Qy      65 VSCGPPGVLLTRPVILAMDHCGEPSPSW 93
      | | | | | : | | | : | | | | | : |
Db      1686 VMCGPHGLKFLKPVELRLPHC---DPKTW 1711
```

RESULT 2

A46431

tight junction-associated protein ZO-1 - mouse

C;Species: Mus musculus (house mouse)

C;Date: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004

C;Accession: A46431

R;Itoh, M.; Nagafuchi, A.; Yonemura, S.; Kitani-Yasuda, T.; Tsukita, S.;

Tsukita, S.

J. Cell Biol. 121, 491-502, 1993

A;Title: The 220-kD protein colocalizing with cadherins in non-epithelial cells is identical to ZO-1, a tight junction-associated protein in epithelial cells: cDNA cloning and immunoelectron microscopy.

A;Reference number: A46431; MUID:93252986; PMID:8486731

A;Accession: A46431

A;Status: preliminary

A;Molecule type: nucleic acid

A;Residues: 1-1745 <ITO>

A;Cross-references: UNIPROT:P39447; GB:D14340; NID:g303709; PIDN:BAA03274.1;

PID:d1003784; PID:g303710

A;Experimental source: F9 cells

A;Note: sequence extracted from NCBI backbone (NCBIN:131200, NCBIP:131201)

F;27-106/Domain: GLGF domain homology <GLG1>

F;428-498/Domain: GLGF domain homology <GLG3>

F;645-794/Domain: guanylate kinase homology <GKI>

Query Match 29.1%; Score 162.5; DB 2; Length 1745;
Best Local Similarity 41.6%; Pred. No. 4.6e-09;
Matches 37; Conservative 12; Mismatches 35; Indels 5; Gaps 2;

```
Qy      7 GTFNFLGGRLMIPNTGISLLIPPDAIPRGKIYEIYLT LHKPEDVRLPL--AGCQTLLSPI 64
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      1635 GIFNSNGGVLSIETGVSIIPQGAIPGIEQEYFKVCRDNSILPPLDKEKGETLLSPL 1694

Qy      65 VSCGPPGVLLTRPVILAMDHCGEPSPSW 93
      | | | | | : | | | : | | | | | : |
Db      1695 VMCGPHGLKFLKPVELRLPHC---DPKTW 1720
```

RESULT 3

T32541

unc-5 protein - *Caenorhabditis elegans*
 C;Species: *Caenorhabditis elegans*
 C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004
 C;Accession: T32541
 R;Latreille, P.
 submitted to the EMBL Data Library, December 1997
 A;Description: The sequence of *C. elegans* cosmid B0273.
 A;Reference number: Z21187
 A;Accession: T32541
 A;Status: preliminary; translated from GB/EMBL/DDBJ
 A;Molecule type: DNA
 A;Residues: 1-919 <LAT>
 A;Cross-references: UNIPROT:O44171; EMBL:AF036698; PIDN:AAB88355.1;
 GSPDB:GN00022; CESP:B0273.4a
 A;Experimental source: strain Bristol N2; clone B0273
 C;Genetics:
 A;Gene: unc-5; CESP:B0273.4a
 A;Map position: 4
 A;Introns: 41/3; 108/1; 142/3; 201/1; 323/2; 553/1; 858/3
 C;Superfamily: unc-5 protein; immunoglobulin homology; SH3 homology;
 thrombospondin type 1 repeat homology

Query Match 17.2%; Score 96; DB 2; Length 919;
 Best Local Similarity 25.7%; Pred. No. 0.034;
 Matches 27; Conservative 21; Mismatches 47; Indels 10; Gaps 3;

```
Qy      1 TSNMTYGTGFNGLGGRIMIPNTGISLLIPPDALPRGKIYEIYLT LHKPEDVRLPLAGCQTL 60
      : | :      : | | : : | | : | :      : | :      : | :
Db      500 SQNIVAAQIDSNGARLSLSKSGARLIVPELAVEGEKM--LYLAVSDTLTDQPHLKPIESA 557

Qy      61 LSPIVSCGPPGV-----LLTRPVILAMDHCGEPS-DSWSLRL 97
      |||:: | |      : | ||::: ' || | | : |
Db      558 LSPVIVIGQCDVSMASHDNILRRPVVVSFRHCASTFPRDNWQFTL 602
```

RESULT 4

B44294

unc-5 protein, long form - *Caenorhabditis elegans*
 N;Contains: unc-5 protein, short form
 C;Species: *Caenorhabditis elegans*
 C;Date: 30-Apr-1993 #sequence_revision 28-Jul-1995 #text_change 09-Jul-2004
 C;Accession: B44294; T32540; A44294
 R;Leung-Hagesteijn, C.; Spence, A.M.; Stern, B.D.; Zhou, Y.; Su, M.W.;
 Hedgecock, E.M.; Culotti, J.G.
 Cell 71, 289-299, 1992
 A;Title: UNC-5, a transmembrane protein with immunoglobulin and thrombospondin
 type 1 domains, guides cell and pioneer axon migrations in *C. elegans*.
 A;Reference number: A44294; MUID:93046629; PMID:1384987
 A;Contents: variety Bergerac
 A;Accession: B44294
 A;Molecule type: DNA
 A;Residues: 1-947 <LEU>
 A;Cross-references: UNIPROT:O44171; GB:S47168; NID:g258527; PIDN:AAB23867.1;
 PID:g258529
 A;Note: sequence extracted from NCBI backbone (NCBIN:116668, NCBIN:116670,
 NCBIN:116672, NCBIN:116674, NCBIN:116676, NCBIN:116678, NCBIN:116680,
 NCBIN:116682, NCBIN:116685, NCBIP:118648)

A;Note: authors translated the codon CTA for residue 642 as Val; sequence shown follows the authors' translation
A;Note: mRNA lacking the first exon is equally prevalent
R;Latreille, P.
submitted to the EMBL Data Library, December 1997
A;Description: The sequence of *C. elegans* cosmid B0273.
A;Reference number: Z21187
A;Accession: T32540
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-947 <LAT>
A;Cross-references: EMBL:AF036698; PIDN:AAB88356.1; GSPDB:GN00022; CESP:B0273.4b
A;Experimental source: strain Bristol N2; clone B0273
C;Genetics:
A;Gene: unc-5
A;Map position: 4
A;Introns: 28/1; 69/3; 136/1; 170/3; 229/1; 351/2; 581/1; 886/3
C;Function:
A;Description: required for guidance of pioneering axons and cells migrating dorsally along the body wall; proposed to be a receptor on the surface of the motile cells
C;Superfamily: unc-5 protein; immunoglobulin homology; SH3 homology; thrombospondin type 1 repeat homology
C;Keywords: alternative splicing; duplication; glycoprotein; receptor; transmembrane protein
F;30-947/Product: unc-5 protein, short form #status predicted <ALT>
F;46-116/Domain: immunoglobulin homology <IM1>
F;153-211/Domain: immunoglobulin homology <IM2>
F;229-300/Domain: thrombospondin type 1 repeat homology #status atypical <THR1>
F;301-354/Domain: thrombospondin type 1 repeat homology <THR2>
F;365-390/Domain: transmembrane #status predicted <TMM>
F;512-559/Domain: SH3 homology <SH3>
F;53-114,65-112,160-209/Disulfide bonds: #status predicted
F;206/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 17.2%; Score 96; DB 1; Length 947;
Best Local Similarity 25.7%; Pred. No. 0.035;
Matches 27; Conservative 21; Mismatches 47; Indels 10; Gaps 3;

```

Qy      1 TSNMTYGTFFNLGGRLMIPNTGISLLIPPDAIPRGKIYEIYLT LHKPEDVRLPLAGCQTL 60
      : | :      : | | : : | | : | :      : | : :
Db      528 SQNIVAAQIDSNGARLSLSKSGARLIVPELAVEGEKM--LYLAVSDTLTDQPHLKPIESA 585

Qy      61 LSPIVSCGPPGV-----LLTRPVILAMDHCGEPSP-DSWSLRL 97
      |||:: | |      : | ||::: || | | : |
Db      586 LSPVIVIGQCDVSMASHDNLRPVVVSFRHCASTFPRDNWQFTL 630

```

RESULT 5
S21265

acetylserotonin O-methyltransferase (EC 2.1.1.4) - chicken
N;Alternate names: hydroxyindole O-methyltransferase
C;Species: *Gallus gallus* (chicken)
C;Date: 07-Apr-1994 #sequence_revision 07-Apr-1994 #text_change 09-Jul-2004
C;Accession: S21265; S22154
R;Voisin, P.; Guerlotte, J.; Bernard, M.; Collin, J.P.; Cogne, M.
Biochem. J. 282, 571-576, 1992

A;Title: Molecular cloning and nucleotide sequence of a cDNA encoding hydroxyindole O-methyltransferase from chicken pineal gland.
A;Reference number: S21265; MUID:92189600; PMID:1372168
A;Accession: S21265
A;Molecule type: mRNA
A;Residues: 1-346 <VOI>
A;Cross-references: UNIPROT:Q92056; EMBL:X62309; NID:g62925; PIDN:CAA44189.1; PID:g62926
C;Superfamily: O-methyltransferase
C;Keywords: melatonin biosynthesis; methyltransferase; S-adenosylmethionine

RESULT 6

ankyrin, erythrocyte - mouse
C;Species: Mus musculus (house mouse)
C;Date: 27-May-1994 #sequence_revision 03-Aug-1995 #text_change 09-Jul-2004
C;Accession: S37771
R;Birkenmeier, C.S.; White, R.A.; Peters, L.L.; Hall, E.J.; Lux, S.E.; Barker, J.E.
J. Biol. Chem. 268, 9533-9540, 1993
A;Title: Complex patterns of sequence variation and multiple 5' and 3' ends are found among transcripts of the erythroid ankyrin gene.
A;Reference number: S37771; MUID:93252825; PMID:8486643
A;Accession: S37771
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-1848 <BIR>
A;Cross-references: UNIPROT:Q61302; EMBL:X69063; NID:g311816; PIDN:CAA48801.1; PID:g311817
C;Superfamily: ankyrin; ankyrin repeat homology
C;Keywords: alternative splicing
F;48-80/Domain: ankyrin repeat homology <AN01>
F;81-113/Domain: ankyrin repeat homology <AN02>
F;114-146/Domain: ankyrin repeat homology <AN03>
F;147-175/Domain: ankyrin repeat homology <AN04>
F;176-208/Domain: ankyrin repeat homology <AN05>
F;209-241/Domain: ankyrin repeat homology <AN06>
F;242-274/Domain: ankyrin repeat homology <AN07>
F;275-307/Domain: ankyrin repeat homology <AN08>
F;308-340/Domain: ankyrin repeat homology <AN09>

F;341-373/Domain: ankyrin repeat homology <AN10>
 F;374-406/Domain: ankyrin repeat homology <AN11>
 F;407-439/Domain: ankyrin repeat homology <AN12>
 F;440-472/Domain: ankyrin repeat homology <AN13>
 F;473-505/Domain: ankyrin repeat homology <AN14>
 F;506-538/Domain: ankyrin repeat homology <AN15>
 F;539-571/Domain: ankyrin repeat homology <AN16>
 F;572-604/Domain: ankyrin repeat homology <AN17>
 F;605-637/Domain: ankyrin repeat homology <AN18>
 F;638-670/Domain: ankyrin repeat homology <AN19>
 F;671-703/Domain: ankyrin repeat homology <AN20>
 F;704-736/Domain: ankyrin repeat homology <AN21>
 F;737-769/Domain: ankyrin repeat homology <AN22>
 F;770-802/Domain: ankyrin repeat homology <AN23>

Query Match 13.1%; Score 73; DB 2; Length 1848;
 Best Local Similarity 33.3%; Pred. No. 22;
 Matches 23; Conservative 11; Mismatches 27; Indels 8; Gaps 3;

Qy 20 NTGISLLIPPD--AIPRGKIYEIYLT LHKPEDVRL--PLAGCQTLLSPIVSCGPPGVLLT 75
 : | : : || | | | | | | : : | | | : | | | : | |
 Db 943 HNGLRVVIPRTCAAPT----RITCRLVKPQKLNTPPPLAEEEGLASRIIALGPTGAQFL 998
 Qy 76 RPVILAMDH 84
 ||| : |
 Db 999 SPVIVEIPH 1007

RESULT 7

I49502

ankyrin - mouse

C;Species: Mus musculus (house mouse)

C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004

C;Accession: I49502

R;White, R.A.; Birkenmeier, C.S.; Peters, L.L.; Barker, J.E.; Lux, S.E.

Mamm. Genome 3, 281-285, 1992

A;Title: Murine erythrocyte ankyrin cDNA: Highly conserved regions of the regulatory domain.

A;Reference number: I49502; MUID:92345717; PMID:1386265

A;Accession: I49502

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: mRNA

A;Residues: 1-1862 <RES>

A;Cross-references: UNIPROT:Q02357; GB:M84756; NID:g191939; PIDN:AAA37236.1; PID:g191940

C;Genetics:

A;Gene: Ank-1

C;Superfamily: ankyrin; ankyrin repeat homology

C;Keywords: alternative splicing

F;40-72/Domain: ankyrin repeat homology <AN01>

F;73-105/Domain: ankyrin repeat homology <AN02>

F;106-138/Domain: ankyrin repeat homology <AN03>

F;139-167/Domain: ankyrin repeat homology <AN04>

F;168-200/Domain: ankyrin repeat homology <AN05>

F;201-233/Domain: ankyrin repeat homology <AN06>

F;234-266/Domain: ankyrin repeat homology <AN07>

F;267-299/Domain: ankyrin repeat homology <AN08>

F;300-332/Domain: ankyrin repeat homology <AN09>
 F;333-365/Domain: ankyrin repeat homology <AN10>
 F;366-398/Domain: ankyrin repeat homology <AN11>
 F;399-431/Domain: ankyrin repeat homology <AN12>
 F;432-464/Domain: ankyrin repeat homology <AN13>
 F;465-497/Domain: ankyrin repeat homology <AN14>
 F;498-530/Domain: ankyrin repeat homology <AN15>
 F;531-563/Domain: ankyrin repeat homology <AN16>
 F;564-596/Domain: ankyrin repeat homology <AN17>
 F;597-629/Domain: ankyrin repeat homology <AN18>
 F;630-662/Domain: ankyrin repeat homology <AN19>
 F;663-695/Domain: ankyrin repeat homology <AN20>
 F;696-728/Domain: ankyrin repeat homology <AN21>
 F;729-761/Domain: ankyrin repeat homology <AN22>
 F;762-794/Domain: ankyrin repeat homology <AN23>

Query Match 13.1%; Score 73; DB 2; Length 1862;
 Best Local Similarity 33.3%; Pred. No. 23;
 Matches 23; Conservative 11; Mismatches 27; Indels 8; Gaps 3;

Qy 20 NTGISLLIPPD--AIPRGKIYEIYLT LHKPEDVRL--PLAGCQTLLSPIVSCGPPGVLLT 75
 : | : : || | | | | | | : | | : | | : | |
 Db 927 HNGLRVVIPRTCAAPT----RITCRLVKPQKLNTPPPLAEEEGLASRIIALGPTGAQFL 982

Qy 76 RPVILAMDH 84
 ||| : |
 Db 983 SPVIVEIPH 991

RESULT 8

B35049

ankyrin 1, erythrocyte splice form 3 - human

N;Alternate names: ankyrin 2.1, erythrocyte; ankyrin-R

N;Contains: ankyrin 2.2, erythrocyte

C;Species: Homo sapiens (man)

C;Date: 17-Nov-1995 #sequence_revision 17-Nov-1995 #text_change 10-Jul-1998

C;Accession: B35049

R;Lambert, S.; Yu, H.; Prchal, J.T.; Lawler, J.; Ruff, P.; Speicher, D.; Cheung, M.C.; Kan, Y.W.; Palek, J.

Proc. Natl. Acad. Sci. U.S.A. 87, 1730-1734, 1990

A;Title: cDNA sequence for human erythrocyte ankyrin.

A;Reference number: A35049; MUID:90175370; PMID:1689849

A;Accession: B35049

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-1856 <LAM>

C;Genetics:

A;Gene: GDB:ANK1; ANK

A;Cross-references: GDB:118737; OMIM:182900

A;Map position: 8p11.2-8p11.2

C;Superfamily: ankyrin; ankyrin repeat homology

C;Keywords: alternative splicing

F;2-1856/Product: ankyrin 1, erythrocyte form 3 #status predicted <MAT>

F;2-1513,1676-1856/Product: ankyrin 2.2, erythrocyte #status predicted <MA2>

F;44-76/Domain: ankyrin repeat homology <AN01>

F;77-109/Domain: ankyrin repeat homology <AN02>

F;110-142/Domain: ankyrin repeat homology <AN03>

F;143-171/Domain: ankyrin repeat homology <AN04>
 F;172-204/Domain: ankyrin repeat homology <AN05>
 F;205-237/Domain: ankyrin repeat homology <AN06>
 F;238-270/Domain: ankyrin repeat homology <AN07>
 F;271-303/Domain: ankyrin repeat homology <AN08>
 F;304-336/Domain: ankyrin repeat homology <AN09>
 F;337-369/Domain: ankyrin repeat homology <AN10>
 F;370-402/Domain: ankyrin repeat homology <AN11>
 F;403-435/Domain: ankyrin repeat homology <AN12>
 F;436-468/Domain: ankyrin repeat homology <AN13>
 F;469-501/Domain: ankyrin repeat homology <AN14>
 F;502-534/Domain: ankyrin repeat homology <AN15>
 F;535-567/Domain: ankyrin repeat homology <AN16>
 F;568-600/Domain: ankyrin repeat homology <AN17>
 F;601-633/Domain: ankyrin repeat homology <AN18>
 F;634-666/Domain: ankyrin repeat homology <AN19>
 F;667-699/Domain: ankyrin repeat homology <AN20>
 F;700-732/Domain: ankyrin repeat homology <AN21>
 F;733-765/Domain: ankyrin repeat homology <AN22>
 F;766-798/Domain: ankyrin repeat homology <AN23>

Query Match 12.9%; Score 72; DB 2; Length 1856;
 Best Local Similarity 33.3%; Pred. No. 29;
 Matches 23; Conservative 11; Mismatches 27; Indels 8; Gaps 3;

Qy 20 NTGISLLIPPD--AIPRGKIYEIYLT LHKPEDVRL--PLAGCQTLLSPIVSCGPPGVLLT 75
 : | : ::||| | | | | | : : ||| : | | | : | |
 Db 931 HNGLRVVIPRTCAAPT----RITCRLVKPQKLSTPPPLAEEEGLASRIIALGPTGAQFL 986
 Qy 76 RPYVILAMDH 84
 ||| : |
 Db 987 SPVIVEIPH 995

RESULT 9

A35049

ankyrin 1, erythrocyte splice form 2 - human

N;Alternate names: ankyrin 2.1, erythrocyte; ankyrin-R

N;Contains: ankyrin 2.2, erythrocyte

C;Species: Homo sapiens (man)

C;Date: 27-Jul-1990 #sequence_revision 01-Oct-1992 #text_change 09-Jul-2004

C;Accession: A35049

R;Lambert, S.; Yu, H.; Prchal, J.T.; Lawler, J.; Ruff, P.; Speicher, D.; Cheung, M.C.; Kan, Y.W.; Palek, J.

Proc. Natl. Acad. Sci. U.S.A. 87, 1730-1734, 1990

A;Title: cDNA sequence for human erythrocyte ankyrin.

A;Reference number: A35049; MUID:90175370; PMID:1689849

A;Accession: A35049

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-1880 <LAM>

A;Cross-references: UNIPROT:P16157; GB:M28880

C;Genetics:

A;Gene: GDB:ANK1; ANK

A;Cross-references: GDB:118737; OMIM:182900

A;Map position: 8p11.2-8p11.2

C;Superfamily: ankyrin; ankyrin repeat homology

C;Keywords: alternative splicing; cytoskeleton
 F;2-1880/Product: ankyrin 1, erythrocyte form 2 #status predicted <MAT>
 F;2-1513,1676-1880/Product: ankyrin 2.2, erythrocyte #status predicted <MA2>
 F;44-76/Domain: ankyrin repeat homology <AN01>
 F;77-109/Domain: ankyrin repeat homology <AN02>
 F;110-142/Domain: ankyrin repeat homology <AN03>
 F;143-171/Domain: ankyrin repeat homology <AN04>
 F;172-204/Domain: ankyrin repeat homology <AN05>
 F;205-237/Domain: ankyrin repeat homology <AN06>
 F;238-270/Domain: ankyrin repeat homology <AN07>
 F;271-303/Domain: ankyrin repeat homology <AN08>
 F;304-336/Domain: ankyrin repeat homology <AN09>
 F;337-369/Domain: ankyrin repeat homology <AN10>
 F;370-402/Domain: ankyrin repeat homology <AN11>
 F;403-435/Domain: ankyrin repeat homology <AN12>
 F;436-468/Domain: ankyrin repeat homology <AN13>
 F;469-501/Domain: ankyrin repeat homology <AN14>
 F;502-534/Domain: ankyrin repeat homology <AN15>
 F;535-567/Domain: ankyrin repeat homology <AN16>
 F;568-600/Domain: ankyrin repeat homology <AN17>
 F;601-633/Domain: ankyrin repeat homology <AN18>
 F;634-666/Domain: ankyrin repeat homology <AN19>
 F;667-699/Domain: ankyrin repeat homology <AN20>
 F;700-732/Domain: ankyrin repeat homology <AN21>
 F;733-765/Domain: ankyrin repeat homology <AN22>
 F;766-798/Domain: ankyrin repeat homology <AN23>

Query Match 12.9%; Score 72; DB 2; Length 1880;
 Best Local Similarity 33.3%; Pred. No. 29;
 Matches 23; Conservative 11; Mismatches 27; Indels 8; Gaps 3;

Qy 20 NTGISLLIPPD--AIPRGKIYEIYLT LHKPEDVRL--PLAGCQTLLSPIVSCGPPGVLLT 75
 : |: ::||| | | | | | | | : | | | : | |
 Db 931 HNGLRVVIPRTCAAPT----RITCRLVKPQKLSTPPPLAEEEGLASRIIALGPTGAQFL 986
 ,
 Qy 76 RPYILAMDH 84
 | | | : |
 Db 987 SPVIVEIPH 995

RESULT 10

SJHUK

ankyrin 1, erythrocyte splice form 1 - human

N;Alternate names: ankyrin 2.1, erythrocyte; ankyrin-R

N;Contains: ankyrin 2.2

C;Species: Homo sapiens (man)

C;Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 09-Jul-2004

C;Accession: S08275; A33219; PC2220; A35443

R;Lux, S.E.; John, K.M.; Bennett, V.

Nature 344, 36-42, 1990

A;Title: Analysis of cDNA for human erythrocyte ankyrin indicates a repeated structure with homology to tissue-differentiation and cell-cycle control proteins.

A;Reference number: S08275; MUID:90158830; PMID:2137557

A;Accession: S08275

A;Molecule type: mRNA

A;Residues: 1-1881 <LU1>

A;Cross-references: UNIPROT:P16157; EMBL:X16609; NID:g28701; PIDN:CAA34610.1; PID:g28702
A;Accession: A33219
A;Molecule type: protein
A;Residues: 2-7, 'X', 9-17, 'X', 19-20, 'T', 22-30; 733-749, 'A', 751-753; 828-833, 'X', 835-855, 'X', 857-859, 'XX', 862-871; 959-1003; 1106-1120, 'XX', 1123-1128; 1149-1172; 1282-1285, 'E', 1287-1288; 1307-1332; 1345-1365, 'X', 1367; 1383-1427; 1601-1630; 1686-1698, 'D', 1700; 1763-1772 <LUX>
A;Note: 845-Arg and 1392-Thr were also found
R;Hermann, J.; Barel, M.; Frade, R.
Biochem. Biophys. Res. Commun. 204, 453-460, 1994
A;Title: Human erythrocyte ankyrin, a cytoskeleton component, generates the p57 membrane proteinase which cleaves C3, the third component of complement.
A;Reference number: PC2220; MUID:95071348; PMID:7526850
A;Accession: PC2220
A;Molecule type: protein
A;Residues: 910-929 <HER>
R;Davis, L.H.; Bennett, V.
J. Biol. Chem. 265, 10589-10596, 1990
A;Title: Mapping the binding sites of human erythrocyte ankyrin for the anion exchanger and spectrin.
A;Reference number: A35443; MUID:90285190; PMID:2141335
A;Accession: A35443
A;Molecule type: protein
A;Residues: 'X', 5, 'X', 7-12; 403-417, 'X', 419-422, 'H', 424, 'LQ'; 797-800, 'L', 802-814; 862-863, 'X', 865-877; 'X', 899-901, 'T', 903-909, 'X', 911-912 <DAV>
C;Genetics:
A;Gene: GDB:ANK1; ANK
A;Cross-references: GDB:118737; OMIM:182900
A;Map position: 8p11.2-8p11.2
C;Superfamily: ankyrin; ankyrin repeat homology
C;Keywords: alternative splicing; phosphoprotein
F;2-1881/Product: ankyrin 1, erythrocyte form 1 #status predicted <MAT1>
F;2-1512,1675-1881/Product: ankyrin 2.2, erythrocyte #status predicted <MAT2>
F;2-827/Domain: 89K #status predicted <DOM1>
F;2-827/Region: anion exchange protein binding
F;44-76/Domain: ankyrin repeat homology <AN01>
F;77-109/Domain: ankyrin repeat homology <AN02>
F;110-142/Domain: ankyrin repeat homology <AN03>
F;143-171/Domain: ankyrin repeat homology <AN04>
F;172-204/Domain: ankyrin repeat homology <AN05>
F;205-237/Domain: ankyrin repeat homology <AN06>
F;238-270/Domain: ankyrin repeat homology <AN07>
F;271-303/Domain: ankyrin repeat homology <AN08>
F;304-336/Domain: ankyrin repeat homology <AN09>
F;337-369/Domain: ankyrin repeat homology <AN10>
F;370-402/Domain: ankyrin repeat homology <AN11>
F;403-435/Domain: ankyrin repeat homology <AN12>
F;436-468/Domain: ankyrin repeat homology <AN13>
F;469-501/Domain: ankyrin repeat homology <AN14>
F;502-534/Domain: ankyrin repeat homology <AN15>
F;535-567/Domain: ankyrin repeat homology <AN16>
F;568-600/Domain: ankyrin repeat homology <AN17>
F;601-633/Domain: ankyrin repeat homology <AN18>
F;634-666/Domain: ankyrin repeat homology <AN19>
F;667-699/Domain: ankyrin repeat homology <AN20>
F;700-732/Domain: ankyrin repeat homology <AN21>

F;733-765/Domain: ankyrin repeat homology <AN22>
F;766-798/Domain: ankyrin repeat homology <AN23>
F;828-1382/Domain: 62K #status predicted <DOM2>
F;828-1382/Region: spectrin binding
F;1383-1881/Domain: 55K #status predicted <DOM3>

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Best Local Similarity 33.3%; Pred. No. 29;
Matches 23; Conservative 11; Mismatches 27; Indels 8; Gaps 3;

Qy 20 NTGISLLIPPD--AIPRGKIYEIYLT LHKPEDVRL--PLAGCQTLLSPIVSCGPPGVLLT 75
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Db 931 HNGLRVVIPRTCAAPT----RITCRLVKPQKLSTPPPLAEEEGLASRIIALGPTGAQFL 986

Qy 76 RPYVILAMDH 84
| | | : |
Db 987 SPVIVEIPH 995

RESULT 11

S73122

carbamoyl phosphate synthase small chain - red alga (*Porphyra purpurea*)
chloroplast

C;Species: chloroplast *Porphyra purpurea*

C;Date: 19-Mar-1997 #sequence_revision 09-May-1997 #text_change 09-Jul-2004

C;Accession: S73122

R;Reith, M.; Munholland, J.

Plant Mol. Biol. Rep. 13, 333-335, 1995

A;Title: Complete nucleotide sequence of the *Porphyra purpurea* chloroplast
genome.

A;Reference number: S73108

A;Accession: S73122

A;Status: preliminary; nucleic acid sequence not shown; translation not shown

A;Molecule type: DNA

A;Residues: 1-384 <REI>

A;Cross-references: UNIPROT:P51201; EMBL:U38804; NID:g1276652; PIDN:AAC08087.1;

PID:g1276667

A;Note: the nucleotide sequence was submitted to the EMBL Data Library, October
1995

C;Genetics:

A;Gene: carA

A;Genome: chloroplast

C;Superfamily: carbamoyl-phosphate synthase (glutamine-hydrolyzing) small chain;
carbamoyl-phosphate synthase (glutamine-hydrolyzing) small chain homology; trpG
homology

C;Keywords: chloroplast

F;9-373/Domain: carbamoyl-phosphate synthase (glutamine-hydrolyzing) small chain
homology <CPS>

F;197-373/Domain: trpG homology <TRG>

F;272/Active site: Cys #status predicted

Query Match 12.5%; Score 70; DB 2; Length 384;
Best Local Similarity 24.3%; Pred. No. 8.1;
Matches 27; Conservative 20; Mismatches 26; Indels 38; Gaps 6;

Qy 17 MIPNTGISLLIPPD--AIP-----RGKIYE-----IYLT LHKPEDVRLPLAG 56
: ||| : : | : : | | | : | : : || |

Db 161 LIPNVTTNIMYDWDEKSLPSWYLADRNREKIYSQLKVIVIDFGVKLNILR----RLATLG 216

Qy 57 CQTL LSP-----IVSCGPPGVLLTRPVILAMDHCGEPSPDSWSLRLKKQ 100
 || : | :|| | :|| : :|| :: :| :

Db 217 CQITVMPASTPTQDILSCKPDGILLS-----NGPGDPSAVNYGIKTVKE 260

RESULT 12

D72240

tRNA guanine transglycosylase - *Thermotoga maritima* (strain MSB8)

C;Species: *Thermotoga maritima*

C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004

C;Accession: D72240

R;Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hickey, E.K.; Peterson, J.D.; Nelson, W.C.; Ketchum, K.A.; McDonald, L.; Utterback, T.R.; Malek, J.A.; Linher, K.D.; Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson, D.; Heidelberg, J.; Sutton, G.G.; Fleischmann, R.D.; White, O.; Salzberg, S.L.; Smith, H.O.; Venter, J.C.; Fraser, C.M.

Nature 399, 323-329, 1999

A;Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome sequence of *Thermotoga maritima*.

A;Reference number: A72200; MUID:99287316; PMID:10360571

A;Accession: D72240

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-369 <ARN>

A;Cross-references: UNIPROT:Q9X1P7; GB:AE001801; GB:AE000512; NID:g4982114; PIDN:AAD36627.1; PID:g4982128; TIGR:TM1561

A;Experimental source: strain MSB8

C;Genetics:

A;Gene: TM1561

C;Superfamily: queuine tRNA-ribosyltransferase

Query Match 12.4%; Score 69.5; DB 2; Length 369;
 Best Local Similarity 23.9%; Pred. No. 8.8;
 Matches 26; Conservative 19; Mismatches 35; Indels 29; Gaps 6;

Qy 7 GTFNFLGGR--LMIPNTGISLLIPPDAIPRGKIYEIYLT LHKPEDV--RLPLAGCQTLLS 62
 | ||:| : :: :| : :||: :| : | | | |:| :| :

Db 75 GLHNFMGWKRPILTDSGGFQVF----SLPKIRIDD-----EGVVFRSPIDGSKVFLN 122

Qy 63 PIVSCGPPGVLLTRPVILAMDHCGEPSPD-----SWSLRLKK 99
 | :| :| : : ||| | | | :||| ||

Db 123 PEISM-EVQIALGSDICMVFDHCPVPDADYEEVKEATERTYRWALRSKK 170

RESULT 13

I48780

Stral/Eplg2 protein - mouse

C;Species: *Mus musculus* (house mouse)

C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004

C;Accession: I48780; A55507; A55062; S52670

R;Bouillet, P.; Oulad-Abdelghani, M.; Vicaire, S.; Garnier, J.M.; Schuhbaur, B.; Dolle, P.; Chambon, P.

Dev. Biol. 170, 420-433, 1995

A;Title: Efficient cloning of cDNAs of retinoic acid-responsive genes in P19 embryonal carcinoma cells and characterization of a novel mouse gene, Stral (mouse LERK-2/Eplg2).

A;Reference number: I48780; MUID:95377533; PMID:7649373

A;Accession: I48780

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: mRNA

A;Residues: 1-345 <RES>

A;Cross-references: UNIPROT:P52795; EMBL:Z48781; NID:g747858; PIDN:CAA88695.1; PID:g747859

R;Fletcher, F.A.; Renshaw, B.; Hollingsworth, T.; Baum, P.; Lyman, S.D.; Jenkins, N.A.; Gilbert, D.J.; Copeland, N.G.; Davison, B.L. Genomics 24, 127-132, 1994

A;Title: Genomic organization and chromosomal localization of mouse Eplg2, a gene encoding a binding protein for the receptor tyrosine kinase Elk.

A;Reference number: A55507; MUID:95203867; PMID:7896266

A;Accession: A55507

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-345 <FLE>

A;Cross-references: GB:U07598

R;Shao, H.; Lou, L.; Pandey, A.; Pasquale, E.B.; Dixit, V.M. J. Biol. Chem. 269, 26606-26609, 1994

A;Title: cDNA cloning and characterization of a ligand for the Cek5 receptor protein-tyrosine kinase.

A;Reference number: A55062; MUID:95014510; PMID:7929389

A;Accession: A55062

A;Status: preliminary; not compared with conceptual translation

A;Molecule type: mRNA

A;Residues: 1-89, 'T', 91-345 <SHA>

A;Cross-references: GB:U12983; NID:g575928; PIDN:AAA53231.1; PID:g575929

C;Genetics:

A;Gene: EPLG2

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 Best Local Similarity 30.9%; Pred. No. 9.3;
 Matches 29; Conservative 11; Mismatches 40; Indels 14; Gaps 5;

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Db      44 FLSGKGLVIYPKIGDKLDIICPRAEAGRPYEYYKLYLVRPEQA----AACSTVLDPNVLV 99

Qy      66 SCGPPGVLLTRPVILAMDHCGEPSDPSWSLRLKK 99
          :|  |  :  :  |  |  |  |  |  |  |  |  |  |  |  |  |  |
Db     100 TCNKPHEIRFTIKFQ-----EFSPNYMGLEFKK 128

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RESULT 14

I58406

LERK-2 - rat

C;Species: Rattus norvegicus (Norway rat)

C;Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 09-Jul-2004

C;Accession: I58406

R;Fletcher, F.A.; Carpenter, M.; Shilling, H.; Baum, P.; Ziegler, S.; Gimpel, S.; Hollingsworth, T.; VandenBos, T.; Davison, B.L.; Lyman, S.D.; Beckmann, M.P. Oncogene 9, 3241-3248, 1994

A;Title: LERK-2, a ligand for the receptor tyrosine kinase ELK, is evolutionarily conserved and expressed in a developmentally regulated pattern.
A;Reference number: I58406; MUID:95022634; PMID:7936648
A;Accession: I58406
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-345 <RES>
A;Cross-references: UNIPROT:P52796; EMBL:U07560; NID:g563118; PIDN:AAA53092.1; PID:g563119
C;Genetics:
A;Gene: Eplg2

Query Match 12.3%; Score 69; DB 2; Length 345;
Best Local Similarity 31.9%; Pred. No. 9.3;
Matches 30; Conservative 10; Mismatches 40; Indels 14; Gaps 5;

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Db      44 FLSGKGLVIYPKIGDKLDIICPRAEAGRPYEYKLYLVRPEQA----AACSTVLDPNVLV 99

Qy      66 SCGPPGVLLTRPVILAMDHCGEPSDWSLRLKK 99
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Db     100 TCNKP-----QQEIRFTIKFQEFSPNYMGLEFKK 128
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RESULT 15

S46993

elk ligand - human

C;Species: Homo sapiens (man)

C;Date: 15-Jul-1995 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004

C;Accession: S46993

R;Beckmann, M.P.; Cerretti, D.P.; Baum, P.; vanden Bos, T.; James, L.; Farrah, T.; Kozlosky, C.; Hollingsworth, T.; Shilling, H.; Maraskovsky, E.; Fletcher, F.A.; Lhotak, V.; Pawson, T.; Lyman, S.D.

EMBO J. 13, 3757-3762, 1994

A;Title: Molecular characterization of a family of ligands for eph-related tyrosine kinase receptors.

A;Reference number: S46993; MUID:94349923; PMID:8070404

A;Accession: S46993

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-346 <BEC>

A;Cross-references: UNIPROT:P98172; GB:U09304; NID:g538366; PIDN:AAA53093.1; PID:g538367

Query Match 12.2%; Score 68; DB 2; Length 346;
Best Local Similarity 30.9%; Pred. No. 12;
Matches 29; Conservative 11; Mismatches 40; Indels 14; Gaps 5;

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          || |: :: | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      44 FLSGKGLVIYPKIGDKLDIICPRAEAGRPYEYKLYLVRPEQA----AACSTVLDPNVLV 99

Qy      66 SCGPPGVLLTRPVILAMDHCGEPSDWSLRLKK 99
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Search completed: March 1, 2005, 09:07:22
Job time : 5.05992 secs

OM protein - protein search, using sw model

Run on: March 1, 2005, 09:06:01 ; Search time 20.0163 Seconds
(without alignments)
1704.439 Million cell updates/sec

Title: US-10-624-932-2_COPY_495_598
Perfect score: 559
Sequence: 1 TSNMTYGTFFNGLGRLMIPN.....CGEPSPDSWSLRLKKQSCEG 104

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1385339 seqs, 328044528 residues

Total number of hits satisfying chosen parameters: 1385339

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications_AA:*

- 1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
- 2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
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- 10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep:*
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- 18: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep:*
- 19: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep:*
- 20: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	559	100.0	544	10	US-09-970-944-14	Sequence 14, Appl
2	559	100.0	842	15	US-10-311-623-1	Sequence 1, Appli
3	559	100.0	898	10	US-09-918-779-2	Sequence 2, Appli
4	559	100.0	898	15	US-10-624-932-2	Sequence 2, Appli
5	559	100.0	899	10	US-09-970-944-2	Sequence 2, Appli
6	555	99.3	436	15	US-10-296-115-1104	Sequence 1104, Ap
7	553	98.9	557	10	US-09-933-261-6	Sequence 6, Appli
8	553	98.9	557	14	US-10-256-702-6	Sequence 6, Appli
9	553	98.9	898	10	US-09-933-261-5	Sequence 5, Appli
10	553	98.9	898	10	US-09-970-944-13	Sequence 13, Appl
11	553	98.9	898	14	US-10-256-702-5	Sequence 5, Appli
12	553	98.9	898	14	US-10-240-154-16	Sequence 16, Appl
13	348	62.3	931	10	US-09-970-944-15	Sequence 15, Appl
14	348	62.3	931	11	US-09-972-211-121	Sequence 121, App
15	348	62.3	931	15	US-10-087-684-35	Sequence 35, Appl
16	348	62.3	931	15	US-10-037-417-117	Sequence 117, App
17	348	62.3	931	15	US-10-096-625-121	Sequence 121, App
18	348	62.3	1010	15	US-10-218-779-35	Sequence 35, Appl
19	337	60.3	931	10	US-09-970-944-16	Sequence 16, Appl
20	337	60.3	931	10	US-09-970-944-17	Sequence 17, Appl
21	337	60.3	931	11	US-09-972-211-122	Sequence 122, App
22	337	60.3	931	11	US-09-972-211-125	Sequence 125, App
23	337	60.3	931	15	US-10-087-684-36	Sequence 36, Appl
24	337	60.3	931	15	US-10-218-779-36	Sequence 36, Appl
25	337	60.3	931	15	US-10-037-417-118	Sequence 118, App
26	337	60.3	931	15	US-10-037-417-119	Sequence 119, App
27	337	60.3	931	15	US-10-037-417-120	Sequence 120, App
28	337	60.3	931	15	US-10-096-625-122	Sequence 122, App
29	337	60.3	931	15	US-10-096-625-125	Sequence 125, App
30	287	51.3	223	9	US-09-764-870-436	Sequence 436, App
31	287	51.3	223	14	US-10-125-540-436	Sequence 436, App
32	287	51.3	554	15	US-10-108-260A-2682	Sequence 2682, Ap
33	287	51.3	933	15	US-10-087-684-2	Sequence 2, Appli
34	287	51.3	933	15	US-10-087-684-4	Sequence 4, Appli
35	287	51.3	933	15	US-10-218-779-2	Sequence 2, Appli
36	287	51.3	933	15	US-10-218-779-4	Sequence 4, Appli
37	287	51.3	945	14	US-10-028-072-146	Sequence 146, App
38	287	51.3	945	14	US-10-140-808-146	Sequence 146, App
39	287	51.3	945	14	US-10-121-049-146	Sequence 146, App
40	287	51.3	945	14	US-10-123-904-146	Sequence 146, App
41	287	51.3	945	14	US-10-140-470-146	Sequence 146, App
42	287	51.3	945	14	US-10-175-746-146	Sequence 146, App
43	287	51.3	945	14	US-10-176-918-146	Sequence 146, App
44	287	51.3	945	14	US-10-176-921-146	Sequence 146, App
45	287	51.3	945	14	US-10-137-865-146	Sequence 146, App

ALIGNMENTS

RESULT 1

US-09-970-944-14

; Sequence 14, Application US/09970944

; Publication No. US20030204052A1

```
; GENERAL INFORMATION:
; APPLICANT: Herrman, John L
; APPLICANT: Rastelli, Luca
; APPLICANT: Shimkets, Richard A
; TITLE OF INVENTION: No. US20030204052A1 Proteins and Nucleic Acids Encoding
Same and
; TITLE OF INVENTION: Antibodies Directed Against these Proteins
; FILE REFERENCE: 21402-138
; CURRENT APPLICATION NUMBER: US/09/970,944
; CURRENT FILING DATE: 2002-05-02
; PRIOR APPLICATION NUMBER: 60/237,862
; PRIOR FILING DATE: 2000-10-04
; NUMBER OF SEQ ID NOS: 62
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 14
; LENGTH: 544
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-970-944-14
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RESULT 2

US-10-311-623-1

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; Sequence 1, Application US/10311623
; Publication No. US20040023244A1
; GENERAL INFORMATION:
; APPLICANT: INCYTE GENOMICS, INC.; GRIFFIN, Jennifer A.
; APPLICANT: KALLICK, Deborah A.; TRIBOULEY, Catherine M.
; APPLICANT: YUE, Henry; NGUYEN, Dannel B.
; APPLICANT: TANG, Y. Tom; LAL, Preeti G.
; APPLICANT: POLICKY, Jennifer L.; AZIMZAI, Yalda
; APPLICANT: LU, Dyung Aina M.; GRAUL, Richard C.
; APPLICANT: YAO, Monique G.; BURFORD, Neil
; APPLICANT: HAFALIA, April J. A.; BAUGHN, Mariah R.
; APPLICANT: BANDMAN, Olga; ARVIZU, Chandra S.
; APPLICANT: YANG, Junming; XU, Yuming
; APPLICANT: GANDHI, Ameena R.; WARREN, Bridget A.
; APPLICANT: DING, Li; SANJANWALA, Madhusudan M.
; APPLICANT: DUGGAN, Brendan M.; LU, Yan
; TITLE OF INVENTION: RECEPTORS
; FILE REFERENCE: PF-0793 USN
; CURRENT APPLICATION NUMBER: US/10/311,623
; CURRENT FILING DATE: 2002-12-17
; PRIOR APPLICATION NUMBER: US 01/19942
; PRIOR FILING DATE: 2001-06-21
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; PRIOR APPLICATION NUMBER: US 60/214,027
; PRIOR FILING DATE: 2000-06-21
; PRIOR APPLICATION NUMBER: US 60/228,045
; PRIOR FILING DATE: 2000-08-25
; PRIOR APPLICATION NUMBER: US 60/255,104
; PRIOR FILING DATE: 2000-12-12
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PERL Program
; SEQ ID NO 1
; LENGTH: 842
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No. US20040023244A1 6052371CD1
US-10-311-623-1
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Qy      1 TSNMTYGTFFNGLGRLMIPNTGISLLIPPDAIPRGKIYEIYLTLLHKPEDVRLPLAGCQTL 60
      |||
Db      439 TSNMTYGTFFNGLGRLMIPNTGISLLIPPDAIPRGKIYEIYLTLLHKPEDVRLPLAGCQTL 498

Qy      61 LSPIVSCGPPGVLLTRPVILAMDHCGEPSDWSLRLKKQSCEG 104
      |||
Db      499 LSPIVSCGPPGVLLTRPVILAMDHCGEPSDWSLRLKKQSCEG 542
```

RESULT 3

US-09-918-779-2

```
; Sequence 2, Application US/09918779
; Publication No. US20030064369A1
; GENERAL INFORMATION:
; APPLICANT: Taupier, Raymond
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Rastelli, Luca
; APPLICANT: Spaderna, Steven
; APPLICANT: Shimkets, Richard
; APPLICANT: Zerhusen, Bryan
; APPLICANT: Spytek, Kimberly
; APPLICANT: Shenoy, Suresh
; APPLICANT: Li, Li
; APPLICANT: Gusev, Vladimir
; APPLICANT: Grosse, William
; APPLICANT: Alsobrook, John
; APPLICANT: Lepley, Denise
; APPLICANT: Burgess, Catherine
; APPLICANT: Gerlach, Valerie
; APPLICANT: Ellerman, Karen
; APPLICANT: MacDougall, John
; APPLICANT: Stone, David
; APPLICANT: Smithson, Glennda
; TITLE OF INVENTION: Novel Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-074 US
; CURRENT APPLICATION NUMBER: US/09/918,779
```

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; CURRENT FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/221,409
; PRIOR FILING DATE: 2000-07-28
; PRIOR APPLICATION NUMBER: 60/222,840
; PRIOR FILING DATE: 2000-08-04
; PRIOR APPLICATION NUMBER: 60/223,752
; PRIOR FILING DATE: 2000-08-08
; PRIOR APPLICATION NUMBER: 60/223,762
; PRIOR FILING DATE: 2000-08-08
; PRIOR APPLICATION NUMBER: 60/223,770
; PRIOR FILING DATE: 2000-08-08
; PRIOR APPLICATION NUMBER: 60/223,769
; PRIOR FILING DATE: 2000-08-08
; PRIOR APPLICATION NUMBER: 60/225,146
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/225,392
; PRIOR FILING DATE: 2000-08-15
; PRIOR APPLICATION NUMBER: 60/225,470
; PRIOR FILING DATE: 2000-08-15
; PRIOR APPLICATION NUMBER: 60/225,697
; PRIOR FILING DATE: 2000-08-16
; PRIOR APPLICATION NUMBER: 60/263,662
; PRIOR FILING DATE: 2001-02-01
; PRIOR APPLICATION NUMBER: 60/281,645
; PRIOR FILING DATE: 2001-04-05
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 898
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-918-779-2
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Query Match          100.0%; Score 559; DB 10; Length 898;
Best Local Similarity 100.0%; Pred. No. 4.9e-56;
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
Qy      1 TSNMTYGTFFNFGGRLMIPNTGISLLIPPDAIPRGKIYEIYLTLLHKPEDVRLPLAGCQTL 60
          |||
Db      495 TSNMTYGTFFNFGGRLMIPNTGISLLIPPDAIPRGKIYEIYLTLLHKPEDVRLPLAGCQTL 554

Qy      61 LSPIVSCGPPGVLLTRPVILAMDHCGEPSDWSLRLKKQSCEG 104
          |||
Db      555 LSPIVSCGPPGVLLTRPVILAMDHCGEPSDWSLRLKKQSCEG 598
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RESULT 4

US-10-624-932-2

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; Sequence 2, Application US/10624932
; Publication No. US20040096877A1
; GENERAL INFORMATION:
; APPLICANT: Taupier, Raymond
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Rastelli, Luca
; APPLICANT: Spaderna, Steven
; APPLICANT: Shimkets, Richard
; APPLICANT: Zerhusen, Bryan
```

```

; APPLICANT: Spytek, Kimberly
; APPLICANT: Shenoy, Suresh
; APPLICANT: Li, Li
; APPLICANT: Gusev, Vladimir
; APPLICANT: Grosse, William
; APPLICANT: Alsobrook, John
; APPLICANT: Lepley, Denise
; APPLICANT: Burgess, Catherine
; APPLICANT: Gerlach, Valerie
; APPLICANT: Ellerman, Karen
; APPLICANT: MacDougall, John
; APPLICANT: Stone, David
; APPLICANT: Smithson, Glennda
; TITLE OF INVENTION: Novel Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-074 US
; CURRENT APPLICATION NUMBER: US/10/624,932
; CURRENT FILING DATE: 2003-07-21
; PRIOR APPLICATION NUMBER: 09/918,779
; PRIOR FILING DATE: 2001-07-03
; PRIOR APPLICATION NUMBER: 60/221,409
; PRIOR FILING DATE: 2000-07-28
; PRIOR APPLICATION NUMBER: 60/222,840
; PRIOR FILING DATE: 2000-08-04
; PRIOR APPLICATION NUMBER: 60/223,752
; PRIOR FILING DATE: 2000-08-08
; PRIOR APPLICATION NUMBER: 60/223,762
; PRIOR FILING DATE: 2000-08-08
; PRIOR APPLICATION NUMBER: 60/223,770
; PRIOR FILING DATE: 2000-08-08
; PRIOR APPLICATION NUMBER: 60/223,769
; PRIOR FILING DATE: 2000-08-08
; PRIOR APPLICATION NUMBER: 60/225,146
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/225,392
; PRIOR FILING DATE: 2000-08-15
; PRIOR APPLICATION NUMBER: 60/225,470
; PRIOR FILING DATE: 2000-08-15
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 898
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-624-932-2

```

```

Query Match          100.0%; Score 559; DB 15; Length 898;
Best Local Similarity 100.0%; Pred. No. 4.9e-56;
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy          1 TSNMTYGTFFNLGGRLMIPNTGISLLIPPDAIPRGKIYEIYLT LHKPEDVRLPLAGCQTL 60
             |||
Db          495 TSNMTYGTFFNLGGRLMIPNTGISLLIPPDAIPRGKIYEIYLT LHKPEDVRLPLAGCQTL 554
             |||

Qy          61 LSPIVSCGPPGVLLTRPVILAMDHCGEPSDPSWSLRLKKQSCEG 104
             |||
Db          555 LSPIVSCGPPGVLLTRPVILAMDHCGEPSDPSWSLRLKKQSCEG 598

```

RESULT 5

US-09-970-944-2

; Sequence 2, Application US/09970944
 ; Publication No. US20030204052A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Herrman, John L
 ; APPLICANT: Rastelli, Luca
 ; APPLICANT: Shimkets, Richard A
 ; TITLE OF INVENTION: No. US20030204052A1el Proteins and Nucleic Acids Encoding Same and
 ; TITLE OF INVENTION: Antibodies Directed Against these Proteins
 ; FILE REFERENCE: 21402-138
 ; CURRENT APPLICATION NUMBER: US/09/970,944
 ; CURRENT FILING DATE: 2002-05-02
 ; PRIOR APPLICATION NUMBER: 60/237,862
 ; PRIOR FILING DATE: 2000-10-04
 ; NUMBER OF SEQ ID NOS: 62
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 2
 ; LENGTH: 899
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-970-944-2

Query Match 100.0%; Score 559; DB 10; Length 899;
 Best Local Similarity 100.0%; Pred. No. 4.9e-56;
 Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TSNMTYGTFFNFLGGRLMIPNTGISLLIPPDAIPRGKIYEIYLTLLHKPEDVRLPLAGCQTL 60
 |||
 Db 495 TSNMTYGTFFNFLGGRLMIPNTGISLLIPPDAIPRGKIYEIYLTLLHKPEDVRLPLAGCQTL 554
 Qy 61 LSPIVSCGPPGVLLTRPVILAMDHCGEPSDWSLRLKKQSCEG 104
 |||
 Db 555 LSPIVSCGPPGVLLTRPVILAMDHCGEPSDWSLRLKKQSCEG 598

RESULT 6

US-10-296-115-1104

; Sequence 1104, Application US/10296115
 ; Publication No. US20040053248A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Hyseq Inc
 ; TITLE OF INVENTION: No. US20040053248A1el Nucleic Acids and Polypeptides
 ; FILE REFERENCE: 784PCT
 ; CURRENT APPLICATION NUMBER: US/10/296,115
 ; CURRENT FILING DATE: 2002-11-18
 ; PRIOR APPLICATION NUMBER: US09/488,725
 ; PRIOR FILING DATE: 2000-01-21
 ; PRIOR APPLICATION NUMBER: US09/552,317
 ; PRIOR FILING DATE: 2000-04-25
 ; NUMBER OF SEQ ID NOS: 1478
 ; SEQ ID NO 1104
 ; LENGTH: 436
 ; TYPE: PRT


```

; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 343-4341
; TELEFAX: (415) 343-4342
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 557 amino acids
; TYPE: amino acid
; STRANDEDNESS: No. US20030059859A1 Relevant
; TOPOLOGY: No. US20030059859A1 Relevant
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-10-256-702-6

```

```

Query Match          98.9%; Score 553; DB 14; Length 557;
Best Local Similarity 99.0%; Pred. No. 1.4e-55;
Matches 103; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

```

Qy      1 TSNMTYGTFFNLGGRLMIPNTGISLLIPPDAIPRGKIYEIYLT LHKPEDVRLPLAGCQTL 60
        |||
Db      153 TSNMTYGTFFNLGGRLMIPNTGISLLIPPDAIPRGKIYEIYLT LHKPEDVRLPLAGCQTL 212

Qy      61 LSPIVSCGPPGVLLTRPVILAMDHCGEPSDPSWSLRLKKQSC EG 104
        |||
Db      213 LSPIVSCGPPGVLLTRPVILAMDHCGEPSDPSWSLALKKQSC EG 256

```

RESULT 9

US-09-933-261-5

```

; Sequence 5, Application US/09933261
; Publication No. US20030040046A1
; GENERAL INFORMATION:
; APPLICANT: Tessier-Lavigne, Marc
; Leonardo, E. David
; Hink, Lindsay
; Masu, Masayuki
; Kazuko, Keino-Masu
; TITLE OF INVENTION: Netrin Receptors
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
; STREET: 268 BUSH STREET, SUITE 3200
; CITY: SAN FRANCISCO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/933,261
; FILING DATE: 20-Aug-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/808,982
; FILING DATE: <Unknown>

```

```

;      ATTORNEY/AGENT INFORMATION:
;      NAME: OSMAN, RICHARD A
;      REGISTRATION NUMBER: 36,627
;      REFERENCE/DOCKET NUMBER: UC96-217
;      TELECOMMUNICATION INFORMATION:
;      TELEPHONE: (415) 343-4341
;      TELEFAX: (415) 343-4342
;      INFORMATION FOR SEQ ID NO: 5:
;      SEQUENCE CHARACTERISTICS:
;      LENGTH: 898 amino acids
;      TYPE: amino acid
;      STRANDEDNESS: No. US20030040046A1 Relevant
;      TOPOLOGY: No. US20030040046A1 Relevant
;      MOLECULE TYPE: peptide
;      SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-09-933-261-5

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Query Match          98.9%;  Score 553;  DB 10;  Length 898;
Best Local Similarity 98.1%;  Pred. No. 2.5e-55;
Matches 102;  Conservative 1;  Mismatches 1;  Indels 0;  Gaps 0;

```

```

Qy      1 TSNMTYGTFFNGLGRLMIPNTGISLLIPPDAIPRGKIYEIYLTLLHKPEDVRLPLAGCQTL 60
      |||||
Db      495 TSNMAYGTFFNGLGRLMIPNTGISLLIPPDAIPRGKIYEIYLTLLHKPEDVRLPLAGCQTL 554

Qy      61 LSPIVSCGPPGVLLTRPVILAMDHCGEPPDSWSLRLKKQSCEG 104
      |||:|||||
Db      555 LSPVVSCGPPGVLLTRPVILAMDHCGEPPDSWSLRLKKQSCEG 598

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RESULT 10

US-09-970-944-13

```

; Sequence 13, Application US/09970944
; Publication No. US20030204052A1
; GENERAL INFORMATION:
; APPLICANT: Herrman, John L
; APPLICANT: Rastelli, Luca
; APPLICANT: Shimkets, Richard A
; TITLE OF INVENTION: No. US20030204052A1el Proteins and Nucleic Acids Encoding
Same and
; TITLE OF INVENTION: Antibodies Directed Against these Proteins
; FILE REFERENCE: 21402-138
; CURRENT APPLICATION NUMBER: US/09/970,944
; CURRENT FILING DATE: 2002-05-02
; PRIOR APPLICATION NUMBER: 60/237,862
; PRIOR FILING DATE: 2000-10-04
; NUMBER OF SEQ ID NOS: 62
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 13
; LENGTH: 898
; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-09-970-944-13

```

```

Query Match          98.9%;  Score 553;  DB 10;  Length 898;
Best Local Similarity 98.1%;  Pred. No. 2.5e-55;
Matches 102;  Conservative 1;  Mismatches 1;  Indels 0;  Gaps 0;

```

Qy 1 TSNMTYGTFFNFGGRLMIPNTGISLLIPPDAIPRGKIYEIYLTLLHKPEDVRLPLAGCQTL 60
 |||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 495 TSNMAYGTFFNFGGRLMIPNTGISLLIPPDAIPRGKIYEIYLTLLHKPEDVRLPLAGCQTL 554
 Qy 61 LSPIVSCGPPGVLLTRPVILAMDHCGEPSDWSLRLKKQSCEG 104
 |||:||||||||||||||||||||||||||||||||||||||
 Db 555 LSPVVSCGPPGVLLTRPVILAMDHCGEPSDWSLRLKKQSCEG 598

RESULT 11

US-10-256-702-5

; Sequence 5, Application US/10256702

; Publication No. US20030059859A1

; GENERAL INFORMATION:

; APPLICANT: Tessier-Lavigne, Marc

; Leonardo, E. David

; Hink, Lindsay

; Masu, Masayuki

; Kazuko, Keino-Masu

; TITLE OF INVENTION: Netrin Receptors

; NUMBER OF SEQUENCES: 8

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP

; STREET: 268 BUSH STREET, SUITE 3200

; CITY: SAN FRANCISCO

; STATE: CALIFORNIA

; COUNTRY: USA

; ZIP: 94104

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/10/256,702

; FILING DATE: 27-Sep-2002

; CLASSIFICATION: <Unknown>

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US/09/933,261

; FILING DATE: 20-Aug-2001

; APPLICATION NUMBER: 08/808,982

; FILING DATE: <Unknown>

; ATTORNEY/AGENT INFORMATION:

; NAME: OSMAN, RICHARD A

; REGISTRATION NUMBER: 36,627

; REFERENCE/DOCKET NUMBER: UC96-217

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (415) 343-4341

; TELEFAX: (415) 343-4342

; INFORMATION FOR SEQ ID NO: 5:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 898 amino acids

; TYPE: amino acid

; STRANDEDNESS: No. US20030059859A1 Relevant

; TOPOLOGY: No. US20030059859A1 Relevant

; MOLECULE TYPE: peptide

SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-10-256-702-5

Query Match 98.9%; Score 553; DB 14; Length 898;
Best Local Similarity 98.1%; Pred. No. 2.5e-55;
Matches 102; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

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Qy      1 TSNMTYGTFFNFLGGRLMIPNTGISLLIPPDAIPRGKIYEIYLTTLHKPEDVRLPLAGCQTL 60
      |||||
Db      495 TSNMAYGTFFNFLGGRLMIPNTGISLLIPPDAIPRGKIYEIYLTTLHKPEDVRLPLAGCQTL 554
      |||||
Qy      61 LSPIVSCGPPGVLLTRPVILAMDHCGEPSPDSSWRLRLKKQSCEG 104
      |||:|||||
Db      555 LSPVVSCGPPGVLLTRPVILAMDHCGEPSPDSSWRLRLKKQSCEG 598

```

RESULT 12

US-10-240-154-16

```

; Sequence 16, Application US/10240154
; Publication No. US20030175741A1
; GENERAL INFORMATION:
; APPLICANT: Cochran et al.
; TITLE OF INVENTION: SCHIZOPHRENIA RELATED GENES
; FILE REFERENCE: CKFW-P01-006
; CURRENT APPLICATION NUMBER: US/10/240,154
; CURRENT FILING DATE: 2001-04-02
; PRIOR APPLICATION NUMBER: PCT/GB01/01486
; PRIOR FILING DATE: 2001-04-02
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 16
;   LENGTH: 898
;   TYPE: PRT
;   ORGANISM: Rattus sp.
US-10-240-154-16

```

Query Match 98.9%; Score 553; DB 14; Length 898;
Best Local Similarity 98.1%; Pred. No. 2.5e-55;
Matches 102; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

```
Qy      1 TSNMTYGTFNFLGGRLMIPNTGISLLIPPDAIPRGKIYEIYLTLHKPEDVRLPLAGCQTL 60
        |||||
Db     495 TSNMAYGTFNFLGGRLMIPNTGISLLIPPDAIPRGKIYEIYLTLHKPEDVRLPLAGCQTL 554

Qy     61 LSPIVSCGPPGVLLTRPVILAMDHCGEPSDWSLRLKKQSCEG 104
        |||:|||||
Db    555 LSPVVS CGPPGVLLTRPVILAMDHCGEPSDWSLRLKKQSCEG 598
```

RESULT 13

US-09-970-944-15

```
; Sequence 15, Application US/09970944
; Publication No. US20030204052A1
; GENERAL INFORMATION:
; APPLICANT: Herrman, John L
; APPLICANT: Rastelli, Luca
; APPLICANT: Shimkets, Richard A
```

; TITLE OF INVENTION: No. US20030204052A1el Proteins and Nucleic Acids Encoding Same and
 ; TITLE OF INVENTION: Antibodies Directed Against these Proteins
 ; FILE REFERENCE: 21402-138
 ; CURRENT APPLICATION NUMBER: US/09/970,944
 ; CURRENT FILING DATE: 2002-05-02
 ; PRIOR APPLICATION NUMBER: 60/237,862
 ; PRIOR FILING DATE: 2000-10-04
 ; NUMBER OF SEQ ID NOS: 62
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 15
 ; LENGTH: 931
 ; TYPE: PRT
 ; ORGANISM: Caenorhabditis elegans
 US-09-970-944-15

Query Match 62.3%; Score 348; DB 10; Length 931;
 Best Local Similarity 58.6%; Pred. No. 2.1e-31;
 Matches 58; Conservative 23; Mismatches 18; Indels 0; Gaps 0;

Qy 6 YGTFNFLGGRLMIPNTGISLLIPDAIPRGKIYEIYLTTLHKPEDVRLPLAGCQTLLSPIV 65
 :||| ||| |:|:|:|:|:| | |:|:|:|:|:|:| |:| |: | |:|:|:
 Db 533 FGTFNSLGGHLIIPNSGVSLIPAGAI PQGRVYEMYVTVHRKENMRPPMEDSQTLLTPVV 592
 Qy 66 SCGPPGVLLTRPVILAMDHCGEPPDSWSLRLKKQSCEG 104
 :|:|:| |:|:|:|:|:| : || :| : | :|:| |:| :|
 Db 593 SCGPPGALLTRPVILTTLHHCADPSTEDWKIQLKNQAVQG 631

RESULT 14

US-09-972-211-121

; Sequence 121, Application US/09972211

; Publication No. US20040048245A1

; GENERAL INFORMATION:

; APPLICANT: Shimkets, Richard A
 ; APPLICANT: Taupier Jr, Raymond J
 ; APPLICANT: Burgess, Catherine E
 ; APPLICANT: Zerhusen, Bryan D
 ; APPLICANT: Mezes, Peter S
 ; APPLICANT: Rastelli, Luca
 ; APPLICANT: Malyankar, Uriel M
 ; APPLICANT: Grosse, William M
 ; APPLICANT: Alsobrook II, John P
 ; APPLICANT: Lepley, Denise M
 ; APPLICANT: Spytek, Kimberly Ann
 ; APPLICANT: Li, Li
 ; APPLICANT: Edinger, Shlomit
 ; APPLICANT: Gerlach, Valerie
 ; APPLICANT: Ellerman, Karen
 ; APPLICANT: MacDougall, John R
 ; APPLICANT: Gunther, Erik
 ; APPLICANT: Millet, Isabelle
 ; APPLICANT: Stone, David J
 ; APPLICANT: Smithson, Glennnda
 ; APPLICANT: Szekeres Jr, Edward S

; TITLE OF INVENTION: No. US20040048245A1el Human Proteins, Polynucleotides Encoding Them And

```
; TITLE OF INVENTION: Methods Of Using The Same
; FILE REFERENCE: 21402-141
; CURRENT APPLICATION NUMBER: US/09/972,211
; CURRENT FILING DATE: 2001-10-05
; PRIOR APPLICATION NUMBER: 60/238,325
; PRIOR FILING DATE: 2000-10-05
; PRIOR APPLICATION NUMBER: 60/238,323
; PRIOR FILING DATE: 2000-10-05
; PRIOR APPLICATION NUMBER: 60/238,400
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: 60/238,397
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: 60/238,401
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: 60/238,379
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: 60/238,402
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: 30/238,384
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: 60/238,373
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: 60/238,372
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: 60/238,383
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: 60/238,382
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: 60/275,892
; PRIOR FILING DATE: 2001-03-14
; PRIOR APPLICATION NUMBER: 60/296,860
; PRIOR FILING DATE: 2001-06-08
; NUMBER OF SEQ ID NOS: 198
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 121
; LENGTH: 931
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-972-211-121
```

```
Query Match          62.3%; Score 348; DB 11; Length 931;
Best Local Similarity 58.6%; Pred. No. 2.1e-31;
Matches 58; Conservative 23; Mismatches 18; Indels 0; Gaps 0;
```

```
Qy      6 YGTFNFLGGRLMIPNTGISLLIPDAIPRGKIYEIYLT LHKPEDVRLPLAGCQTLLSPIV 65
        :|||| ||| |:||||:|:|||| |||:|:|:|:|:|:|:|:| |: | |||:|:|
Db      533 FGTFNSLGGHLIIPNSGVSLIPAGAI PQGRVYEMYVT VHRKENMRPPMEDSQ TLLTPVV 592

Qy      66 SCGPPGVLLTRPVILAMDHCGEPPSPDSWSLRLKKQSCEG 104
        ||||| ||||| | : || :| : | :|| |: |
Db      593 SCGPPGALLTRPVILT LHHCADPSTEDWKIQLKNQAVQG 631
```

```
RESULT 15
US-10-087-684-35
; Sequence 35, Application US/10087684
; Publication No. US20040029116A1
```

```

; GENERAL INFORMATION:
; APPLICANT: Edinger, Shlomit R.
; APPLICANT: MacDougall, John R.
; APPLICANT: Millet, Isabelle
; APPLICANT: Ellerman, Karen
; APPLICANT: Stone, David J.
; APPLICANT: Grosse, William M.
; APPLICANT: Lepley, Denise M.
; APPLICANT: Rieger, Daniel K.
; APPLICANT: Burgess, Cathereine E.
; APPLICANT: Casman, Stacie, J.
; APPLICANT: Spytek, Kimberly A.
; APPLICANT: Boldog, Ferenc L.
; APPLICANT: Li, Li
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Mishra, Vishnu
; APPLICANT: Shenoy, Suresh G.
; APPLICANT: Rastelli, Luca
; APPLICANT: Tchernev, Velizar T.
; APPLICANT: Vernet, Corine A.M.
; APPLICANT: Zerhusen, Bryan D.
; APPLICANT: Malyankar, Uriel M.
; APPLICANT: Guo, Xiaojia
; APPLICANT: Miller, Charles E.
; APPLICANT: Gangolli, Esha A.
; TITLE OF INVENTION: PROTEINS AND NUCLEIC ACIDS ENCODING SAME
; FILE REFERENCE: 21402-214 CIP
; CURRENT APPLICATION NUMBER: US/10/087,684
; CURRENT FILING DATE: 2003-03-10
; PRIOR APPLICATION NUMBER: 60/253,834
; PRIOR FILING DATE: 2000-11-29
; PRIOR APPLICATION NUMBER: 60/250,926
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: 60/264,180
; PRIOR FILING DATE: 2001-01-25
; PRIOR APPLICATION NUMBER: 60/274,194
; PRIOR FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: 60/313,656
; PRIOR FILING DATE: 2001-08-20
; PRIOR APPLICATION NUMBER: 60/327,456
; PRIOR FILING DATE: 2001-10-05
; NUMBER OF SEQ ID NOS: 220
; SOFTWARE: CuraSeqList version 0.1
; SEQ ID NO 35
; LENGTH: 931
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-087-684-35

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Query Match          62.3%; Score 348; DB 15; Length 931;
Best Local Similarity 58.6%; Pred. No. 2.1e-31;
Matches 58; Conservative 23; Mismatches 18; Indels 0; Gaps 0;

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Qy      6 YGTFNFLGGRLMIPNTGISLLIPDAIPRGKIYEIYLT LHKPEDVRLPLAGCQTLLSPIV 65
       :|||| ||| |:||||:|:|||| |::|::|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db     533 FGTFNSLGGHLIIPNSGVSLLIPAGAI PQGRVYEMYVTVHRKENMRPPMEDSQTLTPVV 592

```

Qy 66 SCGPPGVLLTRPVILAMDHCGEPSDWSLRLKKQSCEG 104
 | | | | | | | | | | : | | : | | : | : | | | : : |
Db 593 SCGPPGALLTRPVILTLLHHCADPSTEDWKIQLKNQAVQG 631

Search completed: March 1, 2005, 09:51:32
Job time : 21.0163 secs

GenCore version 5.1.6
 Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: March 1, 2005, 08:41:47 ; Search time 19.025 Seconds
 (without alignments)
 2799.282 Million cell updates/sec

Title: US-10-624-932-2_COPY_495_598
 Perfect score: 559
 Sequence: 1 TSNMTYGTFFNLGGRLMIPN.....CGEPSPDSWSLRLKKQSCGE 104

Scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : UniProt_03:*
 1: uniprot_sprot:*
 2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a
 score greater than or equal to the score of the result being printed,
 and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	559	100.0	842	1	UN5A_HUMAN	Q6zn44 homo sapien
2	554	99.1	898	1	UN5A_MOUSE	Q8kls4 mus musculu
3	553	98.9	898	1	UN5A_RAT	O08721 rattus norv
4	348	62.3	931	1	UN5C_MOUSE	O08747 mus musculu
5	346	61.9	931	1	UN5C_CHICK	Q7t2z5 gallus gall
6	345	61.7	931	1	UN5C_RAT	Q761x5 rattus norv
7	337	60.3	931	1	UN5C_HUMAN	O95185 homo sapien
8	309	55.3	943	1	UN5B_XENLA	Q8jgt4 xenopus lae
9	287	51.3	945	1	UN5B_HUMAN	Q8izj1 homo sapien
10	277	49.6	945	1	UN5B_RAT	O08722 rattus norv
11	274	49.0	945	1	UN5B_MOUSE	Q8kls3 mus musculu
12	245.5	43.9	956	1	UN5D_MOUSE	Q8kls2 mus musculu
13	243.5	43.6	953	1	UN5D_HUMAN	Q6uxz4 homo sapien
14	192	34.3	1267	2	Q68DX9	Q68dx9 homo sapien
15	192	34.3	1769	2	O97758	O97758 canis famil

16	191	34.2	757	2	Q91YW2	Q91yw2	mus musculu
17	184	32.9	1692	2	Q6MZU1	Q6mzu1	homo sapien
18	163.5	29.2	1736	1	ZO1_HUMAN	Q07157	homo sapien
19	162.5	29.1	1745	1	ZO1_MOUSE	P39447	mus musculu
20	155.5	27.8	2134	2	Q7QAT6	Q7qat6	anopheles g
21	145.5	26.0	518	2	Q8IV45	Q8iv45	homo sapien
22	142.5	25.5	1695	2	Q9BKL2	Q9bkl2	hydra atten
23	139.5	25.0	2090	2	Q9VHK3	Q9vhk3	drosophila
24	135.5	24.2	518	2	Q6R653	Q6r653	mus musculu
25	133.5	23.9	876	2	Q7PW78	Q7pw78	anopheles g
26	116	20.8	149	2	Q7YS63	Q7ys63	sus scrofa
27	101.5	18.2	759	2	Q7PW77	Q7pw77	anopheles g
28	98.5	17.6	1109	2	Q8I103	Q8i103	caenorhabdi
29	96	17.2	919	1	UNC5_CAEEL	Q26261	caenorhabdi
30	86	15.4	1072	1	UNC5_DROME	Q95tu8	drosophila
31	80.5	14.4	370	2	Q72J31	Q72j31	thermus the
32	78	14.0	110	2	Q8QN46	Q8qn46	cowpox viru
33	76.5	13.7	715	2	Q8IZW8	Q8izw8	homo sapien
34	76	13.6	230	2	Q6ZQQ7	Q6zqq7	homo sapien
35	76	13.6	258	2	Q7WZ45	Q7wz45	nonomuraea
36	76	13.6	346	1	HIOM_CHICK	Q92056	gallus gall
37	74.5	13.3	374	2	Q6H6C9	Q6h6c9	oryza sativ
38	74	13.2	121	2	Q8JTG1	Q8jtg1	cowpox viru
39	74	13.2	133	2	Q6ZBE3	Q6zbe3	oryza sativ
40	73.5	13.1	1330	2	Q7R3T6	Q7r3t6	giardia lam
41	73	13.1	1098	2	Q61304	Q61304	mus musculu
42	73	13.1	1136	2	Q9N180	Q9n180	bos taurus
43	73	13.1	1848	2	Q61302	Q61302	mus musculu
44	73	13.1	1862	1	ANK1_MOUSE	Q02357	mus musculu
45	72.5	13.0	120	2	Q90XH5	Q90xh5	coturnix co

ALIGNMENTS

RESULT 1

UN5A_HUMAN

ID UN5A_HUMAN STANDARD; PRT; 842 AA.
AC Q6ZN44; Q8TF26; Q96GP4;
DT 25-OCT-2004 (Rel. 45, Created)
DT 25-OCT-2004 (Rel. 45, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Netrin receptor UNC5A precursor (Unc-5 homolog A) (Unc-5 homolog 1).
GN Name=UNC5A; Synonyms=KIAA1976, UNC5H1;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM 2).
RC TISSUE=Brain;
RX PubMed=14702039; DOI=10.1038/ng1285;
RA Ota T., Suzuki Y., Nishikawa T., Otsuki T., Sugiyama T., Irie R.,
RA Wakamatsu A., Hayashi K., Sato H., Nagai K., Kimura K., Makita H.,
RA Sekine M., Obayashi M., Nishi T., Shibahara T., Tanaka T., Ishii S.,
RA Yamamoto J.-I., Saito K., Kawai Y., Isono Y., Nakamura Y.,
RA Nagahari K., Murakami K., Yasuda T., Iwayanagi T., Wagatsuma M.,

RA Shiratori A., Sudo H., Hosoiri T., Kaku Y., Kodaira H., Kondo H.,
 RA Sugawara M., Takahashi M., Kanda K., Yokoi T., Furuya T., Kikkawa E.,
 RA Omura Y., Abe K., Kamihara K., Katsuta N., Sato K., Tanikawa M.,
 RA Yamazaki M., Ninomiya K., Ishibashi T., Yamashita H., Murakawa K.,
 RA Fujimori K., Tanai H., Kimata M., Watanabe M., Hiraoka S., Chiba Y.,
 RA Ishida S., Ono Y., Takiguchi S., Watanabe S., Yosida M., Hotuta T.,
 RA Kusano J., Kanehori K., Takahashi-Fujii A., Hara H., Tanase T.-O.,
 RA Nomura Y., Togiya S., Komai F., Hara R., Takeuchi K., Arita M.,
 RA Imose N., Musashino K., Yuuki H., Oshima A., Sasaki N., Aotsuka S.,
 RA Yoshikawa Y., Matsunawa H., Ichihara T., Shiohata N., Sano S.,
 RA Moriya S., Momiyama H., Satoh N., Takami S., Terashima Y., Suzuki O.,
 RA Nakagawa S., Senoh A., Mizoguchi H., Goto Y., Shimizu F., Wakebe H.,
 RA Hishigaki H., Watanabe T., Sugiyama A., Takemoto M., Kawakami B.,
 RA Yamazaki M., Watanabe K., Kumagai A., Itakura S., Fukuzumi Y.,
 RA Fujimori Y., Komiyama M., Tashiro H., Tanigami A., Fujiwara T.,
 RA Ono T., Yamada K., Fujii Y., Ozaki K., Hirao M., Ohmori Y.,
 RA Kawabata A., Hikiji T., Kobatake N., Inagaki H., Ikema Y., Okamoto S.,
 RA Okitani R., Kawakami T., Noguchi S., Itoh T., Shigeta K., Senba T.,
 RA Matsumura K., Nakajima Y., Mizuno T., Morinaga M., Sasaki M.,
 RA Togashi T., Oyama M., Hata H., Watanabe M., Komatsu T.,
 RA Mizushima-Sugano J., Satoh T., Shirai Y., Takahashi Y., Nakagawa K.,
 RA Okumura K., Nagase T., Nomura N., Kikuchi H., Masuho Y., Yamashita R.,
 RA Nakai K., Yada T., Nakamura Y., Ohara O., Isogai T., Sugano S.;
 RT "Complete sequencing and characterization of 21,243 full-length human
 RT cDNAs.";
 RL Nat. Genet. 36:40-45(2004).
 RN [2]
 RP SEQUENCE FROM N.A. (ISOFORM 3), AND SEQUENCE OF 302-842 FROM N.A.
 RC TISSUE=Brain;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [3]
 RP SEQUENCE OF 624-728 FROM N.A.
 RC TISSUE=Brain;
 RX MEDLINE=21842142; PubMed=11853319;
 RA Nagase T., Kikuno R., Ohara O.;
 RT "Prediction of the coding sequences of unidentified human genes. XXII.
 RT The complete sequences of 50 new cDNA clones which code for large

RT proteins.";
 RL DNA Res. 8:319-327(2001).
 RN [4]
 RP INDUCTION.
 RX PubMed=12598906; DOI=10.1038/ncb943;
 RA Tanikawa C., Matsuda K., Fukuda S., Nakamura Y., Arakawa H.;
 RT "p53RDL1 regulates of p53-dependent apoptosis.";
 RL Nat. Cell Biol. 5:216-223(2003).
 RN [5]
 RP DOWN-REGULATION IN CANCER.
 RX PubMed=12655055; DOI=10.1073/pnas.0738063100;
 RA Thiebault K., Mazelin L., Pays L., Llambi F., Joly M.-O.,
 RA Scoazec J.-Y., Saurin J.-C., Romeo G., Mehlen P.;
 RT "The netrin-1 receptors UNC5H are putative tumor suppressors
 RT controlling cell death commitment.";
 RL Proc. Natl. Acad. Sci. U.S.A. 100:4173-4178(2003).
 CC -!- FUNCTION: Receptor for netrin required for axon guidance. Mediates
 CC axon repulsion of neuronal growth cones in the developing nervous
 CC system upon ligand binding. Axon repulsion in growth cones may be
 CC caused by its association with DCC that may trigger signaling for
 CC repulsion. It also acts as a dependence receptor required for
 CC apoptosis induction when not associated with netrin ligand.
 CC -!- SUBUNIT: Interacts with the cytoplasmic part of DCC. Interacts
 CC with MAGED1. Interacts with PRKCABP, possibly mediating some
 CC interaction with PKC (By similarity).
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein. The interaction
 CC with PRKCABP regulates its surface expression and leads to its
 CC removal from surface of neurons and growth cones (By similarity).
 CC -!- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=3;
 CC Name=1;
 CC IsoId=Q6ZN44-1; Sequence=Displayed;
 CC Note=No experimental confirmation available;
 CC Name=2;
 CC IsoId=Q6ZN44-2; Sequence=VSP_011694, VSP_011695;
 CC Note=No experimental confirmation available;
 CC Name=3;
 CC IsoId=Q6ZN44-3; Sequence=VSP_011693;
 CC Note=No experimental confirmation available;
 CC -!- INDUCTION: By p53/TP53.
 CC -!- DOMAIN: The ZU5 domain mediates the interaction with MAGED1, which
 CC participates in the induction of apoptosis (By similarity).
 CC -!- PTM: Phosphorylated on cytoplasmic tyrosine residues.
 CC Phosphorylated by PKC in vitro (By similarity).
 CC -!- PTM: Proteolytically cleaved by caspases during apoptosis. The
 CC cleavage does not take place when the receptor is associated with
 CC netrin ligand. Its cleavage by caspases is required to induce
 CC apoptosis (By similarity).
 CC -!- MISCELLANEOUS: Down-regulated in multiple cancers including
 CC colorectal, breast, ovary, uterus, stomach, lung, or kidney
 CC cancers.
 CC -!- SIMILARITY: Belongs to the UNC-5 family.
 CC -!- SIMILARITY: Contains 1 death domain.
 CC -!- SIMILARITY: Contains 1 immunoglobulin-like C2-type domain.
 CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
 CC -!- SIMILARITY: Contains 1 TSP type-1 domain.
 CC -!- SIMILARITY: Contains 1 ZU5 domain.

CC -!- CAUTION: Ref.3 sequence differs from that shown due to the
CC presence of introns.

CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
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CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC -----

DR EMBL; AK131380; BAD18531.1; -.
DR EMBL; BC009333; AAH09333.2; -.
DR EMBL; BC033727; -; NOT_ANNOTATED_CDS.
DR EMBL; AB075856; BAB85562.1; ALT_SEQ.
DR Genew; HGNC:12567; UNC5A.
DR MIM; 607869; -.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR000884; TSP1.
DR Pfam; PF00047; ig; 1.
DR Pfam; PF00090; TSP_1; 1.
DR SMART; SM00409; IG; 1.
DR SMART; SM00209; TSP1; 1.
DR PROSITE; PS50017; DEATH_DOMAIN; FALSE_NEG.
DR PROSITE; PS50835; IG_LIKE; 1.
DR PROSITE; PS50092; TSP1; 1.
KW Alternative splicing; Apoptosis; Developmental protein;
KW Immunoglobulin domain; Phosphorylation; Receptor; Signal;
KW Transmembrane.

FT	SIGNAL	1	25	Potential.
FT	CHAIN	26	842	Netrin receptor UNC5A.
FT	DOMAIN	1	306	Extracellular (Potential).
FT	TRANSMEM	307	327	Potential.
FT	DOMAIN	328	842	Cytoplasmic (Potential).
FT	DOMAIN	44	141	Ig-like.
FT	DOMAIN	155	234	Ig-like C2-type.
FT	DOMAIN	242	294	TSP type-1.
FT	DOMAIN	439	542	ZU5.
FT	DOMAIN	761	841	Death.
FT	SITE	340	341	Cleavage (by caspase-3) (By similarity).
FT	SITE	605	623	Interaction with DCC (By similarity).
FT	DISULFID	65	124	By similarity.
FT	DISULFID	170	221	By similarity.
FT	CARBOHYD	107	107	N-linked (GlcNAc. . .) (Potential).
FT	CARBOHYD	218	218	N-linked (GlcNAc. . .) (Potential).
FT	CARBOHYD	287	287	N-linked (GlcNAc. . .) (Potential).
FT	VARSPPLIC	1	97	MAVRPGLWPALLGIVLAAWLRGSGAQQSATVANPVPGANPD
FT				LLPHFLVEPEDVYIVKNKPVLLVCKAVPATQIFFKCNGEWV
FT				RQVDHVIERSTDGSN -> MAGTSERSLISSISQPKAIECF
FT				EVKKKAFLTHGRYHGSGATPPKTKDPKPETFCGQT (in
FT				isoform 3).
FT				/FTId=VSP_011693.
FT	VARSPPLIC	296	301	TASGPE -> SESSLP (in isoform 2).
FT				/FTId=VSP_011694.
FT	VARSPPLIC	302	842	Missing (in isoform 2).
FT				/FTId=VSP_011695.

Query Match 100.0%; Score 559; DB 1; Length 842;
Best Local Similarity 100.0%; Pred. No. 7.7e-52;
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TSNMTYGTFFNLGGRLMIPNTGISLLIPPDAIPRGKIYEIYLTLHKPEDVRLPLAGCQTL 60
 |||||||
Db 439 TSNMTYGTFFNLGGRLMIPNTGISLLIPPDAIPRGKIYEIYLTLHKPEDVRLPLAGCQTL 498

Qy 61 LSPIVSCGPPGVLLTRPVILAMDHCGEPSPDWSLRLKKQSCEG 104
 |||||||
Db 499 LSPIVSCGPPGVLLTRPVILAMDHCGEPSPDWSLRLKKQSCEG 542

UN5A MOUSE

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ID      UN5A_MOUSE; STANDARD; PRT; 898 AA.
AC      Q8K1S4; Q6PEF7; Q80T71;
DT      25-OCT-2004 (Rel. 45, Created)
DT      25-OCT-2004 (Rel. 45, Last sequence update)
DT      25-OCT-2004 (Rel. 45, Last annotation update)
DE      Netrin receptor UNC5A precursor (Unc-5 homolog A) (Unc-5 homolog 1).
GN      Name=Unc5a; Synonyms=Kiaa1976, Unc5h1;
OS      Mus musculus (Mouse).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX      NCBI_TaxID=10090;
RN      [1]
RP      SEQUENCE FROM N.A. (ISOFORM 1), AND TISSUE SPECIFICITY.
RX      MEDLINE=22239710; PubMed=12351186; DOI=10.1016/S0925-4773(02)00248-4;
RA      Engelkamp D.;
RT      "Cloning of three mouse unc-5 genes and their expression patterns at
RT      mid-gestation.";
RL      Mech. Dev. 118:191-197(2002).
RN      [2]
RP      SEQUENCE FROM N.A. (ISOFORM 3).
RC      TISSUE=Brain;
RX      MEDLINE=22579291; PubMed=12693553;
RA      Okazaki N., Kikuno R., Ohara R., Inamoto S., Aizawa H., Yuasa S.,
RA      Nakajima D., Nagase T., Ohara O., Koga H.;
RT      "Prediction of the coding sequences of mouse homologues of KIAA gene:
RT      II. The complete nucleotide sequences of 400 mouse KIAA-homologous
RT      cDNAs identified by screening of terminal sequences of cDNA clones
RT      randomly sampled from size-fractionated libraries.";
RL      DNA Res. 10:35-48(2003).
RN      [3]
RP      SEQUENCE FROM N.A. (ISOFORM 2).
RC      STRAIN=C57BL/6; TISSUE=Brain;
RX      MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA      Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA      Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA      Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA      Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA      Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA      Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA      Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

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RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 CC -!- FUNCTION: Receptor for netrin required for axon guidance. Mediates
 CC axon repulsion of neuronal growth cones in the developing nervous
 CC system upon ligand binding. Axon repulsion in growth cones may be
 CC caused by its association with DCC that may trigger signaling for
 CC repulsion. It also acts as a dependence receptor required for
 CC apoptosis induction when not associated with netrin ligand (By
 CC similarity).
 CC -!- SUBUNIT: Interacts with the cytoplasmic part of DCC. Interacts
 CC with MAGED1. Interacts with PRKCABP, possibly mediating some
 CC interaction with PKC (By similarity).
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein. The interaction
 CC with PRKCABP regulates its surface expression and leads to its
 CC removal from surface of neurons and growth cones (By similarity).
 CC -!- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=3;
 CC Name=1;
 CC IsoId=Q8K1S4-1; Sequence=Displayed;
 CC Name=2;
 CC IsoId=Q8K1S4-2; Sequence=VSP_011697;
 CC Note=No experimental confirmation available;
 CC Name=3;
 CC IsoId=Q8K1S4-3; Sequence=VSP_011696;
 CC Note=No experimental confirmation available;
 CC -!- TISSUE SPECIFICITY: Restricted to central nervous system.
 CC -!- DOMAIN: The ZU5 domain mediates the interaction with MAGED1, which
 CC participates in the induction of apoptosis (By similarity).
 CC -!- PTM: Phosphorylated by PKC in vitro. Phosphorylated on cytoplasmic
 CC tyrosine residues (By similarity).
 CC -!- PTM: Proteolytically cleaved by caspases during apoptosis. The
 CC cleavage does not take place when the receptor is associated with
 CC netrin ligand. Its cleavage by caspases is required to induce
 CC apoptosis (By similarity).
 CC -!- SIMILARITY: Belongs to the UNC-5 family.
 CC -!- SIMILARITY: Contains 1 death domain.
 CC -!- SIMILARITY: Contains 1 immunoglobulin-like C2-type domain.
 CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
 CC -!- SIMILARITY: Contains 2 TSP type-1 domains.
 CC -!- SIMILARITY: Contains 1 ZU5 domain.
 CC -----
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CC -----

DR EMBL; AJ487852; CAD32250.1; -.
DR EMBL; AK122575; BAC65857.1; ALT_INIT.
DR EMBL; BC058084; AAH58084.1; -.
DR HSSP; P07996; 1LSL.
DR MGD; MGI:894682; Unc5a.
DR InterPro; IPR000488; Death.
DR InterPro; IPR011029; DEATH_like.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR000884; TSP1.
DR InterPro; IPR008085; TSP_1.
DR InterPro; IPR000906; ZU5.
DR Pfam; PF00531; Death; 1.
DR Pfam; PF00047; ig; 1.
DR Pfam; PF00090; TSP_1; 2.
DR Pfam; PF00791; ZU5; 1.
DR PRINTS; PR01705; TSP1REPEAT.
DR SMART; SM00005; DEATH; 1.
DR SMART; SM00409; IG; 1.
DR SMART; SM00209; TSP1; 2.
DR SMART; SM00218; ZU5; 1.
DR PROSITE; PS50017; DEATH_DOMAIN; FALSE_NEG.
DR PROSITE; PS50835; IG_LIKE; 1.
DR PROSITE; PS50092; TSP1; 2.
KW Alternative splicing; Apoptosis; Developmental protein;
KW Immunoglobulin domain; Phosphorylation; Receptor; Repeat; Signal;
KW Transmembrane.
FT SIGNAL 1 25 Potential.
FT CHAIN 26 898 Netrin receptor UNC5A.
FT DOMAIN 26 361 Extracellular (Potential).
FT TRANSMEM 362 382 Potential.
FT DOMAIN 383 898 Cytoplasmic (Potential).
FT DOMAIN 44 141 Ig-like.
FT DOMAIN 155 234 Ig-like C2-type.
FT DOMAIN 242 296 TSP type-1 1.
FT DOMAIN 298 350 TSP type-1 2.
FT DOMAIN 495 598 ZU5.
FT DOMAIN 817 897 Death.
FT SITE 396 397 Cleavage (by caspase-3) (By similarity).
FT SITE 661 679 Interaction with DCC (By similarity).
FT DISULFID 65 124 By similarity.
FT DISULFID 170 221 By similarity.
FT CARBOHYD 107 107 N-linked (GlcNAc . . .) (Potential).
FT CARBOHYD 218 218 N-linked (GlcNAc . . .) (Potential).
FT CARBOHYD 343 343 N-linked (GlcNAc . . .) (Potential).
FT VARSPLIC 1 790 Missing (in isoform 3).
FT /FTId=VSP_011696.
FT VARSPLIC 241 296 Missing (in isoform 2).
FT /FTId=VSP_011697.
FT CONFLICT 217 217 A -> P (in Ref. 3).
SQ SEQUENCE 898 AA; 98856 MW; 59F04BA2E196C1DB CRC64;

Query Match 99.1%; Score 554; DB 1; Length 898;
Best Local Similarity 99.0%; Pred. No. 2.9e-51;

Matches 103; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy      1 TSNMTYGTFTNFLGGRLMIPNTGISLLIPPDAIPRGKIYEIYLTTLHKPEDVRLPLAGCQTL 60
      |||||
Db      495 TSNMAYGTFTNFLGGRLMIPNTGISLLIPPDAIPRGKIYEIYLTTLHKPEDVRLPLAGCQTL 554

Qy      61 LSPIVSCGPPGVLLTRPVILAMDHCGEPSDPSWSLRLKKQSCEG 104
      |||||
Db      555 LSPIVSCGPPGVLLTRPVILAMDHCGEPSDPSWSLRLKKQSCEG 598
```

RESULT 3

UN5A_RAT

ID UN5A_RAT STANDARD; PRT; 898 AA.

AC O08721;

DT 25-OCT-2004 (Rel. 45, Created)

DT 25-OCT-2004 (Rel. 45, Last sequence update)

DT 25-OCT-2004 (Rel. 45, Last annotation update)

DE Netrin receptor UNC5A precursor (Unc-5 homolog A) (Unc-5 homolog 1).

GN Name=Unc5a; Synonyms=Unc5h1;

OS Rattus norvegicus (Rat).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

OX NCBI_TaxID=10116;

RN [1]

RP SEQUENCE FROM N.A., FUNCTION, SUBCELLULAR LOCATION, AND TISSUE
RP SPECIFICITY.

RC TISSUE=Ventral spinal cord;

RX MEDLINE=97271897; PubMed=9126742;

RA Leonardo E.D., Hinck L., Masu M., Keino-Masu K., Ackerman S.L.,

RA Tessier-Lavigne M.;

RT "Vertebrate homologues of C. elegans UNC-5 are candidate netrin
RT receptors.";

RL Nature 386:833-838(1997).

RN [2]

RP FUNCTION, AND INTERACTION WITH DCC.

RX PubMed=10399920;

RA Hong K., Hinck L., Nishiyama M., Poo M.-M., Tessier-Lavigne M.,

RA Stein E.;

RT "A ligand-gated association between cytoplasmic domains of UNC5 and

RT DCC family receptors converts netrin-induced growth cone attraction to
RT repulsion.";

RL Cell 97:927-941(1999).

RN [3]

RP TISSUE SPECIFICITY.

RX PubMed=11472849;

RA Barrett C., Guthrie S.;

RT "Expression patterns of the netrin receptor UNC5H1 among developing
RT motor neurons in the embryonic rat hindbrain.";

RL Mech. Dev. 106:163-166(2001).

RN [4]

RP FUNCTION.

RX PubMed=11387206; DOI=10.1093/emboj/20.11.2715;

RA Llambi F., Causeret F., Bloch-Gallego E., Mehlen P.;

RT "Netrin-1 acts as a survival factor via its receptors UNC5H and DCC.";

RL EMBO J. 20:2715-2722(2001).

RN [5]

RP FUNCTION, SUBCELLULAR LOCATION, AND INTERACTION WITH MAGED1.
 RX PubMed=12598531; DOI=10.1074/jbc.M300415200;
 RA Williams M.E., Strickland P., Watanabe K., Hinck L.;
 RT "UNC5H1 induces apoptosis via its juxtamembrane region through an
 RT interaction with NRAGE.";
 RL J. Biol. Chem. 278:17483-17490(2003).
 RN [6]
 RP INTERACTION WITH PRKCABP, PHOSPHORYLATION, AND MUTAGENESIS OF
 RP 896-ALA--CYS-898.
 RX PubMed=14672991; DOI=23/36/11279;
 RA Williams M.E., Wu S.C.-Y., McKenna W.L., Hinck L.;
 RT "Surface expression of the netrin receptor UNC5H1 is regulated through
 RT a protein kinase C-interacting protein/protein kinase-dependent
 RT mechanism.";
 RL J. Neurosci. 23:11279-11288(2003).

CC -!- FUNCTION: Receptor for netrin required for axon guidance. Mediates
 CC axon repulsion of neuronal growth cones in the developing nervous
 CC system upon ligand binding. Axon repulsion in growth cones may be
 CC caused by its association with DCC that may trigger signaling for
 CC repulsion. It also acts as a dependence receptor required for
 CC apoptosis induction when not associated with netrin ligand.
 CC -!- SUBUNIT: Interacts with the cytoplasmic part of DCC. Interacts
 CC with MAGED1. Interacts with PRKCABP, possibly mediating some
 CC interaction with PKC.
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein. The interaction
 CC with PRKCABP regulates its surface expression and leads to its
 CC removal from surface of neurons and growth cones.
 CC -!- TISSUE SPECIFICITY: Mainly expressed in regions of differentiating
 CC neurons. Expressed at early stages of neural tube development in
 CC the ventral spinal cord. In developing hindbrain, it colocalizes
 CC with a number of cranial motor neuron subpopulations from
 CC embryonic E11 to E14, while DCC is expressed by motor neurons at
 CC E12. Also expressed in non-neural structures, such as the basal
 CC plane of the hindbrain and midbrain, in the developing
 CC hypothalamus, thalamus and in the pallidum.
 CC -!- DOMAIN: The ZU5 domain mediates the interaction with MAGED1, which
 CC participates in the induction of apoptosis.
 CC -!- PTM: Phosphorylated on cytoplasmic tyrosine residues (By
 CC similarity). Phosphorylated by PKC in vitro.
 CC -!- PTM: Proteolytically cleaved by caspases during apoptosis. The
 CC cleavage does not take place when the receptor is associated with
 CC netrin ligand. Its cleavage by caspases is required to induce
 CC apoptosis.
 CC -!- SIMILARITY: Belongs to the UNC-5 family.
 CC -!- SIMILARITY: Contains 1 death domain.
 CC -!- SIMILARITY: Contains 1 immunoglobulin-like C2-type domain.
 CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
 CC -!- SIMILARITY: Contains 2 TSP type-1 domains.
 CC -!- SIMILARITY: Contains 1 ZU5 domain.

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CC -----
DR EMBL; U87305; AAB57678.1; -.
DR HSSP; P07996; 1LSL.
DR RGD; 621755; Unc5h1.
DR InterPro; IPR000488; Death.
DR InterPro; IPR011029; DEATH_like.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR000884; TSP1.
DR InterPro; IPR008085; TSP_1.
DR InterPro; IPR000906; ZU5.
DR Pfam; PF00531; Death; 1.
DR Pfam; PF00047; ig; 1.
DR Pfam; PF00090; TSP_1; 2.
DR Pfam; PF00791; ZU5; 1.
DR PRINTS; PR01705; TSP1REPEAT.
DR SMART; SM00005; DEATH; 1.
DR SMART; SM00409; IG; 1.
DR SMART; SM00209; TSP1; 2.
DR SMART; SM00218; ZU5; 1.
DR PROSITE; PS50017; DEATH_DOMAIN; FALSE_NEG.
DR PROSITE; PS50835; IG_LIKE; 1.
DR PROSITE; PS50092; TSP1; 2.
KW Apoptosis; Developmental protein; Immunoglobulin domain;
KW Phosphorylation; Receptor; Repeat; Signal; Transmembrane.
FT SIGNAL 1 25 Potential.
FT CHAIN 26 898 Netrin receptor UNC5A.
FT DOMAIN 26 361 Extracellular (Potential).
FT TRANSMEM 362 382 Potential.
FT DOMAIN 383 898 Cytoplasmic (Potential).
FT DOMAIN 44 141 Ig-like.
FT DOMAIN 155 238 Ig-like C2-type.
FT DOMAIN 242 296 TSP type-1 1.
FT DOMAIN 298 350 TSP type-1 2.
FT DOMAIN 495 598 ZU5.
FT DOMAIN 817 897 Death.
FT SITE 396 397 Cleavage (by caspase-3) (By similarity).
FT SITE 661 679 Interaction with DCC (By similarity).
FT DISULFID 65 124 By similarity.
FT DISULFID 170 221 By similarity.
FT CARBOHYD 107 107 N-linked (GlcNAc. . .) (Potential).
FT CARBOHYD 218 218 N-linked (GlcNAc. . .) (Potential).
FT CARBOHYD 343 343 N-linked (GlcNAc. . .) (Potential).
FT MUTAGEN 896 898 Missing: Abolishes interaction with
FT PRKCABP.
SQ SEQUENCE 898 AA; 98840 MW; 7A3CBCB9E7ACA135 CRC64;

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Query Match 98.9%; Score 553; DB 1; Length 898;
Best Local Similarity 98.1%; Pred. No. 3.8e-51;
Matches 102; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

```

```

Qy 1 TSNMTYGTGFNGLGGRIMIPNTGISLLIPPDALPRGKIYEIYLTLLHKPEDVRLPLAGCQTL 60
    |||||
Db 495 TSNMAYGTGFNGLGGRIMIPNTGISLLIPPDALPRGKIYEIYLTLLHKPEDVRLPLAGCQTL 554

Qy 61 LSPIVSCGPPGVLLTRPVILAMDHCGEPSDPSWSLRLKKQSCEG 104
    |||:|||||

```

RESULT 4

UN5C_MOUSE

ID UN5C_MOUSE STANDARD; PRT; 931 AA.
AC O08747; Q8CD16;
DT 25-OCT-2004 (Rel. 45, Created)
DT 25-OCT-2004 (Rel. 45, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Netrin receptor UNC5C precursor (Unc-5 homolog C) (Unc-5 homolog 3)
DE (Rostral cerebellar malformation protein).
GN Name=Unc5c; Synonyms=Rcm, Unc5h3;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM 1), FUNCTION, DISEASE, AND TISSUE
RP SPECIFICITY.
RC STRAIN=C57B6/SJL;
RX MEDLINE=97271898; PubMed=9126743;
RA Ackerman S.L., Kozak L.P., Przyborski S.A., Rund L.A., Boyer B.B.,
RA Knowles B.B.;
RT "The mouse rostral cerebellar malformation gene encodes an UNC-5-like
RT protein.";
RL Nature 386:838-842(1997).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM 2).
RC STRAIN=C57BL/6J; TISSUE=Testis;
RX MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
RA Nikaido I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,
RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
RA Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
RA Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,
RA Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,
RA Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
RA Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
RA Kanai A., Kawaji H., Kawasaki Y., Kedzierski R.M., King B.L.,
RA Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
RA Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,
RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
RA Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K.,
RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
RA Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,
RA Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L.,
RA Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
RA Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
RA Birney E., Hayashizaki Y.;

RT "Analysis of the mouse transcriptome based on functional annotation of
 RT 60,770 full-length cDNAs.";
 RL Nature 420:563-573(2002).
 RN [3]
 RP FUNCTION, AND TISSUE SPECIFICITY.
 RX PubMed=9389662;
 RA Przyborski S.A., Knowles B.B., Ackerman S.L.;
 RT "Embryonic phenotype of Unc5h3 mutant mice suggests chemorepulsion
 RT during the formation of the rostral cerebellar boundary.";
 RL Development 125:41-50(1998).
 RN [4]
 RP INTERACTION WITH DCC.
 RX PubMed=10399920;
 RA Hong K., Hinck L., Nishiyama M., Poo M.-M., Tessier-Lavigne M.,
 RA Stein E.;
 RT "A ligand-gated association between cytoplasmic domains of UNC5 and
 RT DCC family receptors converts netrin-induced growth cone attraction to
 RT repulsion.";
 RL Cell 97:927-941(1999).
 RN [5]
 RP PHOSPHORYLATION SITE TYR-568, AND MUTAGENESIS OF TYR-568.
 RX PubMed=11533026; DOI=10.1074/jbc.M103872200;
 RA Tong J., Killeen M., Steven R., Binns K.L., Culotti J., Pawson T.;
 RT "Netrin stimulates tyrosine phosphorylation of the UNC-5 family of
 RT netrin receptors and induces Shp2 binding to the RCM cytodomain.";
 RL J. Biol. Chem. 276:40917-40925(2001).
 RN [6]
 RP FUNCTION.
 RX PubMed=12451134; DOI=22/23/10346;
 RA Finger J.H., Bronson R.T., Harris B., Johnson K., Przyborski S.A.,
 RA Ackerman S.L.;
 RT "The netrin 1 receptors Unc5h3 and Dcc are necessary at multiple
 RT choice points for the guidance of corticospinal tract axons.";
 RL J. Neurosci. 22:10346-10356(2002).
 CC -!- FUNCTION: Receptor for netrin required for axon guidance. Mediates
 CC axon repulsion of neuronal growth cones in the developing nervous
 CC system upon ligand binding. Axon repulsion in growth cones may be
 CC caused by its association with DCC that may trigger signaling for
 CC repulsion. Also involved in corticospinal tract axon guidances
 CC independently of DCC. It also acts as a dependence receptor
 CC required for apoptosis induction when not associated with netrin
 CC ligand.
 CC -!- SUBUNIT: Interacts with the cytoplasmic part of DCC.
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).
 CC -!- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=2;
 CC Name=1;
 CC IsoId=O08747-1; Sequence=Displayed;
 CC Name=2;
 CC IsoId=O08747-2; Sequence=VSP_011702;
 CC -!- TISSUE SPECIFICITY: Mainly expressed in regions of differentiating
 CC neurons. Highly expressed in brain and lung. Weakly expressed in
 CC testis, ovary, spleen, thymus and bladder. Expressed at very low
 CC level in kidney, intestine and salivary gland.
 CC -!- PTM: Phosphorylated on different cytoplasmic tyrosine residues.
 CC Phosphorylation of Tyr-568 leads to an interaction with PTPN11
 CC phosphatase, suggesting that its activity is regulated by

CC phosphorylation/dephosphorylation. Tyrosine phosphorylation is
 CC netrin-dependent.
 CC -!- PTM: Proteolytically cleaved by caspases during apoptosis. The
 CC cleavage does not take place when the receptor is associated with
 CC netrin ligand. Its cleavage by caspases is required to induce
 CC apoptosis (By similarity).
 CC -!- DISEASE: Defects in Unc5c are the cause of rostral cerebellar
 CC malformation (Rcm). Rcm is characterized by cerebellar and
 CC midbrain defects, apparently as a result of abnormal neuronal
 CC migration.
 CC -!- SIMILARITY: Belongs to the UNC-5 family.
 CC -!- SIMILARITY: Contains 1 death domain.
 CC -!- SIMILARITY: Contains 1 immunoglobulin-like C2-type domain.
 CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
 CC -!- SIMILARITY: Contains 2 TSP type-1 domains.
 CC -!- SIMILARITY: Contains 1 ZU5 domain.
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 CC -----
 DR EMBL; U72634; AAB54103.1; -.
 DR EMBL; AK031655; BAC27495.1; -.
 DR HSSP; P07996; 1LSL.
 DR MGD; MGI:1095412; Unc5c.
 DR GO; GO:0005886; C:plasma membrane; IC.
 DR GO; GO:0005042; F:netrin receptor activity; IDA.
 DR GO; GO:0005515; F:protein binding; IDA.
 DR GO; GO:0007420; P:brain development; IMP.
 DR GO; GO:0030334; P:regulation of cell migration; IMP.
 DR InterPro; IPR000488; Death.
 DR InterPro; IPR011029; DEATH_like.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003598; Ig_c2.
 DR InterPro; IPR000884; TSP1.
 DR InterPro; IPR008085; TSP_1.
 DR InterPro; IPR000906; ZU5.
 DR Pfam; PF00531; Death; 1.
 DR Pfam; PF00047; ig; 1.
 DR Pfam; PF00090; TSP_1; 2.
 DR Pfam; PF00791; ZU5; 1.
 DR PRINTS; PR01705; TSP1REPEAT.
 DR SMART; SM00005; DEATH; 1.
 DR SMART; SM00408; IGc2; 1.
 DR SMART; SM00209; TSP1; 2.
 DR SMART; SM00218; ZU5; 1.
 DR PROSITE; PS50017; DEATH_DOMAIN; FALSE_NEG.
 DR PROSITE; PS50835; IG_LIKE; 1.
 DR PROSITE; PS50092; TSP1; 2.
 KW Alternative splicing; Apoptosis; Developmental protein;
 KW Immunoglobulin domain; Phosphorylation; Receptor; Repeat; Signal;
 KW Transmembrane.
 FT SIGNAL 1 40 Potential.

FT	CHAIN	41	931	Netrin receptor UNC5C.
FT	DOMAIN	41	380	Extracellular (Potential).
FT	TRANSMEM	381	401	Potential.
FT	DOMAIN	402	931	Cytoplasmic (Potential).
FT	DOMAIN	62	159	Ig-like.
FT	DOMAIN	161	256	Ig-like C2-type.
FT	DOMAIN	260	314	TSP type-1 1.
FT	DOMAIN	316	368	TSP type-1 2.
FT	DOMAIN	528	631	ZU5.
FT	DOMAIN	850	929	Death.
FT	SITE	415	416	Cleavage (by caspase-3) (By similarity).
FT	SITE	694	712	Interaction with DCC (By similarity).
FT	DISULFID	83	142	By similarity.
FT	DISULFID	188	239	By similarity.
FT	MOD_RES	568	568	Phosphotyrosine.
FT	CARBOHYD	236	236	N-linked (GlcNAc. . .) (Potential).
FT	CARBOHYD	361	361	N-linked (GlcNAc. . .) (Potential).
FT	VARSPLIC	370	370	A -> GFIYPISTEHRPQNEYGFSS (in isoform 2).
FT				/FTId=VSP_011702.
FT	MUTAGEN	568	568	Y->F: Abolishes interaction with PTPN11,
FT				leading to a increased level of
FT				phosphorylation.
FT	CONFLICT	16	16	L -> I (in Ref. 2).
FT	CONFLICT	733	733	H -> R (in Ref. 2).
FT	CONFLICT	924	924	S -> Y (in Ref. 2).
SQ	SEQUENCE	931 AA;	103062 MW;	8A5D951A4EECA179 CRC64;

Query Match 62.3%; Score 348; DB 1; Length 931;
 Best Local Similarity 58.6%; Pred. No. 7.6e-29;
 Matches 58; Conservative 23; Mismatches 18; Indels 0; Gaps 0;

Qy	6	YGTFNFLGGRLMIPNTGISLLIPDAIPRGKIYEIYLT LHKPEDVRLPLAGCQTLLSPIV	65
		: : : : : : : : : : : : : : : : :	
Db	533	FGTFNSLGGHLIIPNSGVSLIPAGAI PQGRVYEMYVT VHRKENMRPPMEDSQTLLTPVV	592
Qy	66	SCGPPGVLLTRPVILAMDHCGEPPSDSWSLRLKKQSCEG	104
		: : : : : :	
Db	593	SCGPPGALLTRPVILT LHHCADPSTEDWKIQLKNQAVQG	631

RESULT 5

UN5C_CHICK

ID UN5C_CHICK STANDARD; PRT; 931 AA.
 AC Q7T2Z5;
 DT 25-OCT-2004 (Rel. 45, Created)
 DT 25-OCT-2004 (Rel. 45, Last sequence update)
 DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DE Netrin receptor UNC5C precursor (Unc-5 homolog C) (Unc-5 homolog 3)
 DE (cUNC-5H3).
 GN Name=UNC5C;
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 OX NCBI_TaxID=9031;
 RN [1]
 RP SEQUENCE FROM N.A., AND TISSUE SPECIFICITY.

```

RX PubMed=12799087;
RA Guan W., Condic M.L.;
RT "Characterization of Netrin-1, Neogenin and cUNC-5H3 expression during
RT chick dorsal root ganglia development.";
RL Gene Expr. Patterns 3:369-373(2003).
CC -!- FUNCTION: Receptor for netrin required for axon guidance. Mediates
CC axon repulsion of neuronal growth cones in the developing nervous
CC system upon ligand binding (By similarity).
CC -!- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).
CC -!- TISSUE SPECIFICITY: Restricted to proprioceptive neurons.
CC -!- PTM: Phosphorylated on cytoplasmic tyrosine residues (By
CC similarity).
CC -!- SIMILARITY: Belongs to the UNC-5 family.
CC -!- SIMILARITY: Contains 1 death domain.
CC -!- SIMILARITY: Contains 1 immunoglobulin-like C2-type domain.
CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
CC -!- SIMILARITY: Contains 2 TSP type-1 domains.
CC -!- SIMILARITY: Contains 1 ZU5 domain.
CC -----
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CC -----
DR EMBL; AY187310; AAC67275.1; -.
DR InterPro; IPR000488; Death.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003598; Ig_c2.
DR InterPro; IPR000884; TSP1.
DR InterPro; IPR000906; ZU5.
DR Pfam; PF00531; Death; 1.
DR Pfam; PF00047; ig; 1.
DR Pfam; PF00090; TSP_1; 2.
DR Pfam; PF00791; ZU5; 1.
DR SMART; SM00005; DEATH; 1.
DR SMART; SM00408; IGc2; 1.
DR SMART; SM00209; TSP1; 2.
DR SMART; SM00218; ZU5; 1.
DR PROSITE; PS50017; DEATH_DOMAIN; FALSE_NEG.
DR PROSITE; PS50835; IG_LIKE; 1.
DR PROSITE; PS50092; TSP1; 2.
KW Developmental protein; Immunoglobulin domain; Phosphorylation;
KW Receptor; Repeat; Signal; Transmembrane.
FT SIGNAL 1 39 Potential.
FT CHAIN 40 931 Netrin receptor UNC5C.
FT DOMAIN 40 380 Extracellular (Potential).
FT TRANSMEM 381 401 Potential.
FT DOMAIN 402 931 Cytoplasmic (Potential).
FT DOMAIN 62 159 Ig-like.
FT DOMAIN 161 256 Ig-like C2-type.
FT DOMAIN 260 314 TSP type-1 1.
FT DOMAIN 316 368 TSP type-1 2.
FT DOMAIN 528 631 ZU5.
FT DOMAIN 850 929 Death.

```

FT DISULFID 83 142 By similarity.
 FT DISULFID 188 239 By similarity.
 FT CARBOHYD 236 236 N-linked (GlcNAc. . .) (Potential).
 FT CARBOHYD 361 361 N-linked (GlcNAc. . .) (Potential).
 SQ SEQUENCE 931 AA; 102906 MW; 1E23A0D84F2E2C62 CRC64;

Query Match 61.9%; Score 346; DB 1; Length 931;
 Best Local Similarity 58.6%; Pred. No. 1.3e-28;
 Matches 58; Conservative 22; Mismatches 19; Indels 0; Gaps 0;

Qy 6 YGTFNFLGGRLMIPNTGISLLIPDAIPRGKIYEIYLT LHKPEDVRLPLAGCQTLLSPIV 65
 :||| | | :|||:|:| | | | | :|:|:|:|:|:|:| | :| | : | | | :|:
 Db 533 FGTFNSLGGHLVIPNSGVSLIPAGAVPQGRVYEMVTVHRKEGM RPPVEDSQTLLTPVV 592

Qy 66 SCGPPGVLLTRPVILAMDHCGEPSPD SWSLRLKKQSCEG 104
 ||||| |||||:| | || ||: | | :|| | : |
 Db 593 SCGPPGALLTRPVVLTMHCAEPNMDDWQIQ LKHQAGQG 631

RESULT 6

UN5C_RAT

ID UN5C_RAT STANDARD; PRT; 931 AA.

AC Q761X5;

DT 25-OCT-2004 (Rel. 45, Created)

DT 25-OCT-2004 (Rel. 45, Last sequence update)

DT 25-OCT-2004 (Rel. 45, Last annotation update)

DE Netrin receptor UNC5C precursor (Unc-5 homolog C) (Unc-5 homolog 3).

GN Name=Unc5c; Synonyms=Unc5h3;

OS Rattus norvegicus (Rat).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

OX NCBI_TaxID=10116;

RN [1]

RP SEQUENCE FROM N.A., AND DISEASE.

RX PubMed=15010202; DOI=10.1016/j.molbrainres.2003.12.003;

RA Kuramoto T., Kuwamura M., Serikawa T.;

RT "Rat neurological mutations cerebellar vermis defect and hobble are caused by mutations in the netrin-1 receptor gene Unc5h3.";

RL Brain Res. Mol. Brain Res. 122:103-108(2004).

RN [2]

RP FUNCTION.

RX PubMed=11387206; DOI=10.1093/emboj/20.11.2715;

RA Llambi F., Causeret F., Bloch-Gallego E., Mehlen P.;

RT "Netrin-1 acts as a survival factor via its receptors UNC5H and DCC.";

RL EMBO J. 20:2715-2722(2001).

CC -!- FUNCTION: Receptor for netrin required for axon guidance. Mediates axon repulsion of neuronal growth cones in the developing nervous system upon ligand binding. Axon repulsion in growth cones may be caused by its association with DCC that may trigger signaling for repulsion. Also involved in corticospinal tract axon guidances independently of DCC. It also acts as a dependence receptor required for apoptosis induction when not associated with netrin ligand.

CC -!- SUBUNIT: Interacts with the cytoplasmic part of DCC (By similarity).

CC -!- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).

CC -!- TISSUE SPECIFICITY: Mainly expressed in brain. Also expressed in

CC kidney. Not expressed in developing or adult lung.
 CC -!- PTM: Phosphorylated on different cytoplasmic tyrosine residues.
 CC Phosphorylation of Tyr-568 leads to an interaction with PTPN11
 CC phosphatase, suggesting that its activity is regulated by
 CC phosphorylation/dephosphorylation. Tyrosine phosphorylation is
 CC netrin-dependent (By similarity).
 CC -!- PTM: Proteolytically cleaved by caspases during apoptosis. The
 CC cleavage does not take place when the receptor is associated with
 CC netrin ligand. Its cleavage by caspases is required to induce
 CC apoptosis.
 CC -!- DISEASE: Defects in Unc5c are the cause of cerebellar vermis
 CC defect (cvd) and hobble (hob) phenotypes. Cvd and hob rats exhibit
 CC cerebellar and midbrain defects, possibly as a result of abnormal
 CC neuronal migration, and exhibit laminar structure abnormalities in
 CC the fused cerebellar hemispheres and ectopic cerebellar tissues in
 CC the cerebello-pontine junction.
 CC -!- SIMILARITY: Belongs to the UNC-5 family.
 CC -!- SIMILARITY: Contains 1 death domain.
 CC -!- SIMILARITY: Contains 1 immunoglobulin-like C2-type domain.
 CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
 CC -!- SIMILARITY: Contains 2 TSP type-1 domains.
 CC -!- SIMILARITY: Contains 1 ZU5 domain.
 CC -----
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 CC -----
 DR EMBL; AB118026; BAD05181.1; -.
 DR RGD; 735109; Unc5c.
 DR InterPro; IPR000488; Death.
 DR InterPro; IPR011029; DEATH_like.
 DR InterPro; IPR003599; Ig.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003598; Ig_c2.
 DR InterPro; IPR000884; TSP1.
 DR InterPro; IPR008085; TSP_1.
 DR InterPro; IPR000906; ZU5.
 DR Pfam; PF00531; Death; 1.
 DR Pfam; PF00047; ig; 1.
 DR Pfam; PF00090; TSP_1; 2.
 DR Pfam; PF00791; ZU5; 1.
 DR PRINTS; PR01705; TSP1REPEAT.
 DR SMART; SM00005; DEATH; 1.
 DR SMART; SM00409; IG; 1.
 DR SMART; SM00408; IGc2; 1.
 DR SMART; SM00209; TSP1; 2.
 DR SMART; SM00218; ZU5; 1.
 DR PROSITE; PS50017; DEATH_DOMAIN; FALSE_NEG.
 DR PROSITE; PS50835; IG_LIKE; 1.
 DR PROSITE; PS50092; TSP1; 2.
 KW Apoptosis; Developmental protein; Immunoglobulin domain;
 KW Phosphorylation; Receptor; Repeat; Signal; Transmembrane.
 FT SIGNAL 1 40 Potential.

FT	CHAIN	41	931	Netrin receptor UNC5C.
FT	DOMAIN	41	380	Extracellular (Potential).
FT	TRANSMEM	381	401	Potential.
FT	DOMAIN	402	931	Cytoplasmic (Potential).
FT	DOMAIN	62	159	Ig-like.
FT	DOMAIN	161	256	Ig-like C2-type.
FT	DOMAIN	260	314	TSP type-1 1.
FT	DOMAIN	316	368	TSP type-1 2.
FT	DOMAIN	528	631	ZU5.
FT	DOMAIN	850	929	Death.
FT	SITE	415	416	Cleavage (by caspase-3) (By similarity).
FT	SITE	694	712	Interaction with DCC (By similarity).
FT	DISULFID	83	142	By similarity.
FT	DISULFID	188	239	By similarity.
FT	MOD_RES	568	568	Phosphotyrosine (By similarity).
FT	CARBOHYD	236	236	N-linked (GlcNAc. . .) (Potential).
FT	CARBOHYD	361	361	N-linked (GlcNAc. . .) (Potential).
SQ	SEQUENCE	931 AA;	103134 MW;	25B183A97BCB8401 CRC64;

RESULT 7

RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [3]
 RP DOWN-REGULATION IN CANCER.
 RX PubMed=12655055; DOI=10.1073/pnas.0738063100;
 RA Thiebault K., Mazelin L., Pays L., Llambi F., Joly M.-O.,
 RA Scoazec J.-Y., Saurin J.-C., Romeo G., Mehlen P.;
 RT "The netrin-1 receptors UNC5H are putative tumor suppressors
 RT controlling cell death commitment.";
 RL Proc. Natl. Acad. Sci. U.S.A. 100:4173-4178(2003).
 CC -!- FUNCTION: Receptor for netrin required for axon guidance. Mediates
 CC axon repulsion of neuronal growth cones in the developing nervous
 CC system upon ligand binding. Axon repulsion in growth cones may be
 CC caused by its association with DCC that may trigger signaling for
 CC repulsion. Also involved in corticospinal tract axon guidances
 CC independently of DCC. It also acts as a dependence receptor
 CC required for apoptosis induction when not associated with netrin
 CC ligand (By similarity).
 CC -!- SUBUNIT: Interacts with the cytoplasmic part of DCC (By
 CC similarity).
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).
 CC -!- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=2;
 CC Name=1;
 CC IsoId=O95185-1; Sequence=Displayed;
 CC Name=2;
 CC IsoId=O95185-2; Sequence=VSP_011700, VSP_011701;
 CC -!- TISSUE SPECIFICITY: Mainly expressed in brain. Also expressed in
 CC kidney. Not expressed in developing or adult lung.
 CC -!- PTM: Phosphorylated on different cytoplasmic tyrosine residues.
 CC Phosphorylation of Tyr-568 leads to an interaction with PTPN11
 CC phosphatase, suggesting that its activity is regulated by
 CC phosphorylation/dephosphorylation. Tyrosine phosphorylation is
 CC netrin-dependent (By similarity).
 CC -!- PTM: Proteolytically cleaved by caspases during apoptosis. The
 CC cleavage does not take place when the receptor is associated with
 CC netrin ligand. Its cleavage by caspases is required to induce
 CC apoptosis (By similarity).
 CC -!- MISCELLANEOUS: Down-regulated in multiple cancers including
 CC colorectal, breast, ovary, uterus, stomach, lung, or kidney

CC cancers.

CC -!- SIMILARITY: Belongs to the UNC-5 family.

CC -!- SIMILARITY: Contains 1 death domain.

CC -!- SIMILARITY: Contains 1 immunoglobulin-like C2-type domain.

CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.

CC -!- SIMILARITY: Contains 2 TSP type-1 domains.

CC -!- SIMILARITY: Contains 1 ZU5 domain.

CC -----

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CC -----

DR EMBL; AF055634; AAC67491.1; -.

DR EMBL; BC041156; AAH41156.1; -.

DR HSSP; P07996; 1LSL.

DR Genew; HGNC:12569; UNC5C.

DR MIM; 603610; -.

DR GO; GO:0005042; F:netrin receptor activity; TAS.

DR GO; GO:0007411; P:axon guidance; TAS.

DR GO; GO:0007420; P:brain development; TAS.

DR InterPro; IPR000488; Death.

DR InterPro; IPR011029; DEATH_like.

DR InterPro; IPR007110; Ig-like.

DR InterPro; IPR003598; Ig_c2.

DR InterPro; IPR000884; TSP1.

DR InterPro; IPR008085; TSP_1.

DR InterPro; IPR000906; ZU5.

DR Pfam; PF00531; Death; 1.

DR Pfam; PF00047; ig; 1.

DR Pfam; PF00090; TSP_1; 2.

DR Pfam; PF00791; ZU5; 1.

DR PRINTS; PR01705; TSP1REPEAT.

DR SMART; SM00005; DEATH; 1.

DR SMART; SM00408; IGc2; 1.

DR SMART; SM00209; TSP1; 2.

DR SMART; SM00218; ZU5; 1.

DR PROSITE; PS50017; DEATH_DOMAIN; FALSE_NEG.

DR PROSITE; PS50835; IG_LIKE; 1.

DR PROSITE; PS50092; TSP1; 2.

KW Alternative splicing; Apoptosis; Developmental protein;

KW Immunoglobulin domain; Phosphorylation; Polymorphism; Receptor;

KW Repeat; Signal; Transmembrane.

FT	SIGNAL	1	40	Potential.
FT	CHAIN	41	931	Netrin receptor UNC5C.
FT	DOMAIN	41	380	Extracellular (Potential).
FT	TRANSMEM	381	401	Potential.
FT	DOMAIN	402	931	Cytoplasmic (Potential).
FT	DOMAIN	62	159	Ig-like.
FT	DOMAIN	161	256	Ig-like C2-type.
FT	DOMAIN	260	314	TSP type-1 1.
FT	DOMAIN	316	368	TSP type-1 2.
FT	DOMAIN	528	631	ZU5.
FT	DOMAIN	850	929	Death.

FT	SITE	415	416	Cleavage (by caspase-3) (By similarity).
FT	SITE	694	712	Interaction with DCC (By similarity).
FT	DISULFID	83	142	By similarity.
FT	DISULFID	188	239	By similarity.
FT	MOD_RES	568	568	Phosphotyrosine (By similarity).
FT	CARBOHYD	236	236	N-linked (GlcNAc. . .) (Potential).
FT	CARBOHYD	361	361	N-linked (GlcNAc. . .) (Potential).
FT	VARSPPLIC	370	370	T -> SFIYPISTEQRTQNEYGFSS (in isoform 2).
FT				/FTId=VSP_011700.
FT	VARSPPLIC	579	931	Missing (in isoform 2).
FT				/FTId=VSP_011701.
FT	VARIANT	37	37	G -> V (in dbSNP:2306715).
FT				/FTId=VAR_019731.
FT	VARIANT	721	721	T -> M (in dbSNP:2289043).
FT				/FTId=VAR_019732.
FT	CONFLICT	219	219	T -> I (in Ref. 1).
FT	CONFLICT	489	489	S -> T (in Ref. 1).
SQ	SEQUENCE	931 AA;	103101 MW;	EFD71122C98DABB8 CRC64;

Query Match 60.3%; Score 337; DB 1; Length 931;
 Best Local Similarity 55.6%; Pred. No. 1.2e-27;
 Matches 55; Conservative 24; Mismatches 20; Indels 0; Gaps 0;

Qy	6	YGTFNFLGGRLMIPNTGISLLIPDAIPRGKIYEIYLT LHKPEDVRLPLAGCQTLLSPIV	65
		: : : : : :	
Db	533	FGSFNSLGGHLIVPNSGVSLIPAGAI PQGRVYEMYVT VHRKETMRPPMDDSQTLLTPVV	592
Qy	66	SCGPPGVLLTRPVILAMDHCGEPSDWSLRLKKQSC	104
Db	593	SCGPPGALLTRPVVLTMHHCADPNTEDWKILLKNQAAQ	631

RESULT 8

UN5B_XENLA

ID UN5B_XENLA STANDARD; PRT; 943 AA.
 AC Q8JGT4;
 DT 25-OCT-2004 (Rel. 45, Created)
 DT 25-OCT-2004 (Rel. 45, Last sequence update)
 DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DE Netrin receptor UNC5B precursor (UNC-5 homolog) (Protein XUNC-5).
 OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
 OC Xenopodinae; Xenopus.
 OX NCBI_TaxID=8355;
 RN [1]
 RP SEQUENCE FROM N.A., AND TISSUE SPECIFICITY.
 RX MEDLINE=22239703; PubMed=12351179; DOI=10.1016/S0925-4773(02)00215-0;
 RA Anderson R.B., Holt C.E.;
 RT "Expression of UNC-5 in the developing Xenopus visual system."
 RL Mech. Dev. 118:157-160(2002).
 CC -!- FUNCTION: Receptor for netrin required for axon guidance. Mediates
 CC axon repulsion of neuronal growth cones in the developing nervous
 CC system upon ligand binding (By similarity).
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).
 CC -!- TISSUE SPECIFICITY: In the developing visual system, it is
 CC expressed within the developing optic vesicles and later become

CC restricted to the dorsal ciliary marginal zone, a site of
 CC retinoblast proliferation and differentiation.
 CC -!- PTM: Phosphorylated on cytoplasmic tyrosine residues (By
 CC similarity).
 CC -!- SIMILARITY: Belongs to the UNC-5 family.
 CC -!- SIMILARITY: Contains 1 death domain.
 CC -!- SIMILARITY: Contains 1 immunoglobulin-like C2-type domain.
 CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
 CC -!- SIMILARITY: Contains 2 TSP type-1 domains.
 CC -!- SIMILARITY: Contains 1 ZU5 domain.
 CC -----
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 CC -----
 DR EMBL; AY099459; AAM34486.1; -.
 DR HSSP; P07996; 1LSL.
 DR InterPro; IPR000488; Death.
 DR InterPro; IPR011029; DEATH_like.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003598; Ig_c2.
 DR InterPro; IPR000884; TSP1.
 DR InterPro; IPR008085; TSP_1.
 DR InterPro; IPR000906; ZU5.
 DR Pfam; PF00531; Death; 1.
 DR Pfam; PF00047; ig; 1.
 DR Pfam; PF00090; TSP_1; 2.
 DR Pfam; PF00791; ZU5; 1.
 DR PRINTS; PR01705; TSP1REPEAT.
 DR SMART; SM00005; DEATH; 1.
 DR SMART; SM00408; IGc2; 1.
 DR SMART; SM00209; TSP1; 2.
 DR SMART; SM00218; ZU5; 1.
 DR PROSITE; PS50017; DEATH_DOMAIN; FALSE_NEG.
 DR PROSITE; PS50835; IG_LIKE; 1.
 DR PROSITE; PS50092; TSP1; 2.
 KW Developmental protein; Immunoglobulin domain; Phosphorylation;
 KW Receptor; Repeat; Signal; Transmembrane.
 FT SIGNAL 1 30 Potential.
 FT CHAIN 31 943 Netrin receptor UNC5B.
 FT DOMAIN 31 380 Extracellular (Potential).
 FT TRANSMEM 381 401 Potential.
 FT DOMAIN 402 943 Cytoplasmic (Potential).
 FT DOMAIN 51 148 Ig-like.
 FT DOMAIN 150 245 Ig-like C2-type.
 FT DOMAIN 249 303 TSP type-1 1.
 FT DOMAIN 305 357 TSP type-1 2.
 FT DOMAIN 540 643 ZU5.
 FT DOMAIN 863 941 Death.
 FT DISULFID 72 131 By similarity.
 FT DISULFID 177 228 By similarity.
 FT CARBOHYD 225 225 N-linked (GlcNAc . .) (Potential).
 FT CARBOHYD 350 350 N-linked (GlcNAc . .) (Potential).

SO SEQUENCE 943 AA; 105083 MW; A024E24A7EDB6175` CRC64;

Qy 1 TSNMFTYGTFFNFLGGRLMIPNTGISLLIPPDAIPRGKIYEIYLT LHKHPEDVRLPLAGCQTL 60
:|| ||| ||||| ||||:|||| |||:| ||:| |::| |: || | ||:
Db 540 SSNSVTGTFGSLGGRLTFPNTGVSLLI PQGAI PQGKY YEMYLMINKRENTVLPSEGTQTI 599

Qy 61 LSPIVSCGPPGVLLTRPVILAMDHCGEPSDPSWLR LKKQSCGE 104
||||:|||| |:|| :|||| : || : : | |:|| || :|
Db 600 LSPIITCGPTGLLLCKPVILTVPHCADINTSDWILOLKTOSHOG 643

RESULT 9

```

ID UN5B_HUMAN; STANDARD; PRT; 945 AA.
AC Q8IZJ1; Q86SN3; Q8N1Y2; Q9H9F3;
DT 25-OCT-2004 (Rel. 45, Created)
DT 25-OCT-2004 (Rel. 45, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Netrin receptor UNC5B precursor (Unc-5 homolog B) (Unc-5 homolog 2)
DE (p53-regulated receptor for death and life protein 1)
DE (UNQ1883/PRO4326).
GN Name=UNC5B; Synonyms=P53RDL1, UNC5H2;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM 2), TISSUE SPECIFICITY, AND INTERACTION
RP WITH GNAI2.
RC TISSUE=Lung;
RX MEDLINE=22246081; PubMed=12359238; DOI=10.1016/S0006-291X(02)02277-5;
RA Komatsuzaki K., Dalvin S., Kinane T.B.;
RT "Modulation of G(ialpha(2)) signaling by the axonal guidance molecule
RT UNC5H2.";
RL Biochem. Biophys. Res. Commun. 297:898-905(2002).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM 1), FUNCTION, AND MUTAGENESIS OF ASP-412.
RX PubMed=12598906; DOI=10.1038/ncb943;
RA Tanikawa C., Matsuda K., Fukuda S., Nakamura Y., Arakawa H.;
RT "p53RDL1 regulates of p53-dependent apoptosis.";
RL Nat. Cell Biol. 5:216-223(2003).
RN [3]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RX MEDLINE=22887296; PubMed=12975309; DOI=10.1101/gr.1293003;
RA Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D., Brush J.,
RA Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,
RA Eaton D., Foster J., Grimaldi C., Gu Q., Hass P.E., Heldens S.,
RA Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,
RA Lewis L., Liao D., Mark M., Robbie E., Sanchez C., Schoenfeld J.,
RA Seshagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A.,
RA Vandlen R., Watanabe C., Wieand D., Woods K., Xie M.-H., Yansura D.,
RA Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I.,
RA Godowski P., Gray A.;

```

RT "The secreted protein discovery initiative (SPDI), a large-scale
RT effort to identify novel human secreted and transmembrane proteins: a
RT bioinformatics assessment.";
RL Genome Res. 13:2265-2270(2003).
RN [4]
RP SEQUENCE OF 361-945 FROM N.A.
RC TISSUE=Amygdala, and Teratocarcinoma;
RX PubMed=14702039; DOI=10.1038/ngl285;
RA Ota T., Suzuki Y., Nishikawa T., Otsuki T., Sugiyama T., Irie R.,
RA Wakamatsu A., Hayashi K., Sato H., Nagai K., Kimura K., Makita H.,
RA Sekine M., Obayashi M., Nishi T., Shibahara T., Tanaka T., Ishii S.,
RA Yamamoto J.-I., Saito K., Kawai Y., Isono Y., Nakamura Y.,
RA Nagahari K., Murakami K., Yasuda T., Iwayanagi T., Wagatsuma M.,
RA Shiratori A., Sudo H., Hosoiri T., Kaku Y., Kodaira H., Kondo H.,
RA Sugawara M., Takahashi M., Kanda K., Yokoi T., Furuya T., Kikkawa E.,
RA Omura Y., Abe K., Kamihara K., Katsuta N., Sato K., Tanikawa M.,
RA Yamazaki M., Ninomiya K., Ishibashi T., Yamashita H., Murakawa K.,
RA Fujimori K., Tanai H., Kimata M., Watanabe M., Hiraoka S., Chiba Y.,
RA Ishida S., Ono Y., Takiguchi S., Watanabe S., Yosida M., Hotuta T.,
RA Kusano J., Kanehori K., Takahashi-Fujii A., Hara H., Tanase T.-O.,
RA Nomura Y., Togiya S., Komai F., Hara R., Takeuchi K., Arita M.,
RA Imose N., Musashino K., Yuuki H., Oshima A., Sasaki N., Aotsuka S.,
RA Yoshikawa Y., Matsunawa H., Ichihara T., Shiohata N., Sano S.,
RA Moriya S., Momiyama H., Satoh N., Takami S., Terashima Y., Suzuki O.,
RA Nakagawa S., Senoh A., Mizoguchi H., Goto Y., Shimizu F., Wakebe H.,
RA Hishigaki H., Watanabe T., Sugiyama A., Takemoto M., Kawakami B.,
RA Yamazaki M., Watanabe K., Kumagai A., Itakura S., Fukuzumi Y.,
RA Fujimori Y., Komiyama M., Tashiro H., Tanigami A., Fujiwara T.,
RA Ono T., Yamada K., Fujii Y., Ozaki K., Hirao M., Ohmori Y.,
RA Kawabata A., Hikiji T., Kobatake N., Inagaki H., Ikema Y., Okamoto S.,
RA Okitani R., Kawakami T., Noguchi S., Itoh T., Shigeta K., Senba T.,
RA Matsumura K., Nakajima Y., Mizuno T., Morinaga M., Sasaki M.,
RA Togashi T., Oyama M., Hata H., Watanabe M., Komatsu T.,
RA Mizushima-Sugano J., Satoh T., Shirai Y., Takahashi Y., Nakagawa K.,
RA Okumura K., Nagase T., Nomura N., Kikuchi H., Masuho Y., Yamashita R.,
RA Nakai K., Yada T., Nakamura Y., Ohara O., Isogai T., Sugano S.;
RT "Complete sequencing and characterization of 21,243 full-length human
RT cDNAs.";
RL Nat. Genet. 36:40-45(2004).
RN [5]
RP DOWN-REGULATION IN CANCER.
RX PubMed=12655055; DOI=10.1073/pnas.0738063100;
RA Thiebault K., Mazelin L., Pays L., Llambi F., Joly M.-O.,
RA Scoazec J.-Y., Saurin J.-C., Romeo G., Mehlen P.;
RT "The netrin-1 receptors UNC5H are putative tumor suppressors
RT controlling cell death commitment.";
RL Proc. Natl. Acad. Sci. U.S.A. 100:4173-4178(2003).
CC -!- FUNCTION: Receptor for netrin required for axon guidance. Mediates
CC axon repulsion of neuronal growth cones in the developing nervous
CC system upon ligand binding. Axon repulsion in growth cones may be
CC caused by its association with DCC that may trigger signaling for
CC repulsion. It also acts as a dependence receptor required for
CC apoptosis induction when not associated with netrin ligand.
CC -!- SUBUNIT: Interacts with the cytoplasmic part of DCC (By
CC similarity). Interacts with GNAI2 via its cytoplasmic part.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).
CC -!- ALTERNATIVE PRODUCTS:

CC Event=Alternative splicing; Named isoforms=2;
 CC Name=1;
 CC IsoId=Q8IZJ1-1; Sequence=Displayed;
 CC Name=2;
 CC IsoId=Q8IZJ1-2; Sequence=VSP_011698;
 CC -!- TISSUE SPECIFICITY: Highly expressed in brain. Also expressed at
 CC lower level in developing lung, cartilage, kidney and
 CC hematopoietic and immune tissues.
 CC -!- INDUCTION: By p53/TP53.
 CC -!- PTM: Phosphorylated on cytoplasmic tyrosine residues (By
 CC similarity).
 CC -!- PTM: Proteolytically cleaved by caspases during apoptosis. The
 CC cleavage does not take place when the receptor is associated with
 CC netrin ligand. Its cleavage by caspases is required to induce
 CC apoptosis.
 CC -!- MISCELLANEOUS: Down-regulated in multiple cancers including
 CC colorectal, breast, ovary, uterus, stomach, lung, or kidney
 CC cancers.
 CC -!- SIMILARITY: Belongs to the UNC-5 family.
 CC -!- SIMILARITY: Contains 1 death domain.
 CC -!- SIMILARITY: Contains 1 immunoglobulin-like C2-type domain.
 CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
 CC -!- SIMILARITY: Contains 2 TSP type-1 domains.
 CC -!- SIMILARITY: Contains 1 ZU5 domain.

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 CC -----

DR EMBL; AY126437; AAM95701.1; -.
 DR EMBL; AB096256; BAC57998.1; -.
 DR EMBL; AY358351; AAQ88717.1; -.
 DR EMBL; AK022859; BAB14276.1; ALT_INIT.
 DR EMBL; AK094595; BAC04382.1; ALT_INIT.
 DR HSSP; P07996; 1LSL.
 DR Genew; HGNC:12568; UNC5B.
 DR MIM; 607870; -.
 DR InterPro; IPR000488; Death.
 DR InterPro; IPR011029; DEATH_like.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003598; Ig_c2.
 DR InterPro; IPR000884; TSP1.
 DR InterPro; IPR008085; TSP_1.
 DR InterPro; IPR000906; ZU5.
 DR Pfam; PF00531; Death; 1.
 DR Pfam; PF00047; ig; 1.
 DR Pfam; PF00090; TSP_1; 2.
 DR Pfam; PF00791; ZU5; 1.
 DR PRINTS; PR01705; TSP1REPEAT.
 DR SMART; SM00005; DEATH; 1.
 DR SMART; SM00408; IGc2; 1.
 DR SMART; SM00209; TSP1; 2.
 DR SMART; SM00218; ZU5; 1.

DR PROSITE; PS50017; DEATH_DOMAIN; FALSE_NEG.
 DR PROSITE; PS50835; IG_LIKE; 1.
 DR PROSITE; PS50092; TSP1; 2.
 KW Alternative splicing; Apoptosis; Developmental protein;
 KW Immunoglobulin domain; Phosphorylation; Polymorphism; Receptor;
 KW Repeat; Signal; Transmembrane.
 FT SIGNAL 1 26 Potential.
 FT CHAIN 27 945 Netrin receptor UNC5B.
 FT DOMAIN 27 377 Extracellular (Potential).
 FT TRANSMEM 378 398 Potential.
 FT DOMAIN 399 945 Cytoplasmic (Potential).
 FT DOMAIN 48 145 Ig-like.
 FT DOMAIN 147 242 Ig-like C2-type.
 FT DOMAIN 246 300 TSP type-1 1.
 FT DOMAIN 302 354 TSP type-1 2.
 FT DOMAIN 541 644 ZU5.
 FT DOMAIN 865 943 Death.
 FT SITE 412 413 Cleavage (by caspase-3).
 FT SITE 707 725 Interaction with DCC (By similarity).
 FT DISULFID 69 128 By similarity.
 FT DISULFID 174 225 By similarity.
 FT CARBOHYD 222 222 N-linked (GlcNAc. . .) (Potential).
 FT CARBOHYD 347 347 N-linked (GlcNAc. . .) (Potential).
 FT VARSPLIC 356 367 NKKTLSDPNSHL -> M (in isoform 2).
 FT /FTId=VSP_011698.
 FT VARIANT 516 516 A -> T (in dbSNP:10509332).
 FT /FTId=VAR_019730.
 FT MUTAGEN 412 412 D->N: Abolishes cleavage by caspase-3 and
 subsequent induction of apoptosis.
 FT CONFLICT 483 483 K -> E (in Ref. 3).
 FT CONFLICT 851 851 L -> P (in Ref. 3; BAB14276).
 SQ SEQUENCE 945 AA; 103637 MW; 56064E335F323447 CRC64;

Query Match 51.3%; Score 287; DB 1; Length 945;
 Best Local Similarity 58.6%; Pred. No. 3.3e-22;
 Matches 58; Conservative 13; Mismatches 26; Indels 2; Gaps 2;

Qy 7 GTFNFLGGRLMIPNTGISLLIPPDAIPRGKIYEIYLT LHKPEDVRLPLA-GCQTLLSPIV 65
 ||| |||| | | | : || : | || : || || : || : | | || : | || : || |
 Db 547 GTFGCLGGRLSIPGTGVSLLPNGAIPQGFYEMYLLINKAEST-LPLSEGTQTVLSPSV 605
 Qy 66 SCGPPGVLLTRPVILAMDHCGEPPDSWSLRLKKQSCEG 104
 : || | : || || || | | | | | : || | : : |
 Db 606 TCGPTGLLLCRPVILTMPHCAEVSARDWIFQLKTQAHQG 644

RESULT 10

UN5B_RAT

ID UN5B_RAT STANDARD; PRT; 945 AA.
 AC O08722;
 DT 25-OCT-2004 (Rel. 45, Created)
 DT 25-OCT-2004 (Rel. 45, Last sequence update)
 DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DE Netrin receptor UNC5B precursor (Unc-5 homolog B) (Unc-5 homolog 2).
 GN Name=Unc5b; Synonyms=Unc5h2;
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;

RN [1]

RP SEQUENCE FROM N.A., FUNCTION, SUBCELLULAR LOCATION, AND TISSUE
RP SPECIFICITY.

RX MEDLINE=97271897; PubMed=9126742;

RA Leonardo E.D., Hinck L., Masu M., Keino-Masu K., Ackerman S.L.,

RA Tessier-Lavigne M.;

RT "Vertebrate homologues of *C. elegans* UNC-5 are candidate netrin

RT receptors.";

RL Nature 386:833-838(1997).

RN [2]

RP FUNCTION, AND INTERACTION WITH DCC.

RX PubMed=10399920;

RA Hong K., Hinck L., Nishiyama M., Poo M.-M., Tessier-Lavigne M.,

RA Stein E.;

RT "A ligand-gated association between cytoplasmic domains of UNC5 and

RT DCC family receptors converts netrin-induced growth cone attraction to

RT repulsion.";

RL Cell 97:927-941(1999).

RN [3]

RP FUNCTION, AND MUTAGENESIS OF ASP-412.

RX PubMed=11387206; DOI=10.1093/emboj/20.11.2715;

RA Llambi F., Causeret F., Bloch-Gallego E., Mehlen P.;

RT "Netrin-1 acts as a survival factor via its receptors UNC5H and DCC.";

RL EMBO J. 20:2715-2722(2001).

CC -!- FUNCTION: Receptor for netrin required for axon guidance. Mediates
CC axon repulsion of neuronal growth cones in the developing nervous
CC system upon ligand binding. Axon repulsion in growth cones may be
CC caused by its association with DCC that may trigger signaling for
CC repulsion. It also acts as a dependence receptor required for
CC apoptosis induction when not associated with netrin ligand.

CC -!- SUBUNIT: Interacts with GNAI2 via its cytoplasmic part (By
CC similarity). Interacts with the cytoplasmic part of DCC.

CC -!- SUBCELLULAR LOCATION: Type I membrane protein.

CC -!- TISSUE SPECIFICITY: Mainly expressed in regions of differentiating
CC neurons. Expressed in the developing sensory ganglia that flank
CC the spinal cord from E12, peaking at E14. Expressed in the roof
CC plate region of the spinal cord from E14.

CC -!- PTM: Phosphorylated on cytoplasmic tyrosine residues (By
CC similarity).

CC -!- PTM: Proteolytically cleaved by caspases during apoptosis. The
CC cleavage does not take place when the receptor is associated with
CC netrin ligand. Its cleavage by caspases is required to induce
CC apoptosis.

CC -!- SIMILARITY: Belongs to the UNC-5 family.

CC -!- SIMILARITY: Contains 1 death domain.

CC -!- SIMILARITY: Contains 1 immunoglobulin-like C2-type domain.

CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.

CC -!- SIMILARITY: Contains 2 TSP type-1 domains.

CC -!- SIMILARITY: Contains 1 ZU5 domain.

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CC -----

DR EMBL; U87306; AAB57679.1; -.
DR HSSP; P07996; 1LSL.
DR RGD; 621756; Unc5h2.
DR InterPro; IPR000488; Death.
DR InterPro; IPR011029; DEATH_like.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003598; Ig_c2.
DR InterPro; IPR000884; TSP1.
DR InterPro; IPR008085; TSP_1.
DR InterPro; IPR000906; ZU5.
DR Pfam; PF00531; Death; 1.
DR Pfam; PF00047; ig; 1.
DR Pfam; PF00090; TSP_1; 2.
DR Pfam; PF00791; ZU5; 1.
DR PRINTS; PR01705; TSP1REPEAT.
DR SMART; SM00005; DEATH; 1.
DR SMART; SM00408; IGc2; 1.
DR SMART; SM00209; TSP1; 2.
DR SMART; SM00218; ZU5; 1.
DR PROSITE; PS50017; DEATH_DOMAIN; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
DR PROSITE; PS50092; TSP1; 2.

KW Apoptosis; Developmental protein; Immunoglobulin domain;
KW Phosphorylation; Receptor; Repeat; Signal; Transmembrane.

FT	SIGNAL	1	26	Potential.
FT	CHAIN	27	945	Netrin receptor UNC5B.
FT	DOMAIN	27	377	Extracellular (Potential).
FT	TRANSMEM	378	398	Potential.
FT	DOMAIN	399	945	Cytoplasmic (Potential).
FT	DOMAIN	48	145	Ig-like.
FT	DOMAIN	153	242	Ig-like C2-type.
FT	DOMAIN	246	300	TSP type-1 1.
FT	DOMAIN	302	354	TSP type-1 2.
FT	DOMAIN	541	644	ZU5.
FT	DOMAIN	865	943	Death.
FT	SITE	412	413	Cleavage (by caspase-3).
FT	SITE	707	725	Interaction with DCC.
FT	DISULFID	69	128	By similarity.
FT	DISULFID	174	225	By similarity.
FT	CARBOHYD	222	222	N-linked (GlcNAc. . .) (Potential).
FT	CARBOHYD	347	347	N-linked (GlcNAc. . .) (Potential).
FT	MUTAGEN	412	412	D->N: Abolishes cleavage by caspase-3 and subsequent induction of apoptosis.
FT				
SQ	SEQUENCE	945 AA;	103520 MW;	6E9C2A262E560B9B CRC64;

Query Match 49.6%; Score 277; DB 1; Length 945;
Best Local Similarity 52.9%; Pred. No. 4.1e-21;
Matches 55; Conservative 17; Mismatches 30; Indels 2; Gaps 2;

Qy 2 SNMTYGTFFNGLGGRLMIPNTGISLLIPDAIPRGKIYEIYLTLLHKPEDVRLPLA-GCQTL 60
|: ||| |||| | ||: ||: | ||: || |: || |: | ||: | ||:
Db 542 SSSVSGTFGCLGGRLTIPGTGVSLLPNGAIPQGKFYDLYLRINKTEST-LPLSEGSQTV 600
Qy 61 LSPIVSCGPPGVLLTRPVILAMDHCGEPPSPDSWSLRLKKQSCEG 104

RESULT 11

UN5B_MOUSE

ID UN5B_MOUSE STANDARD; PRT; 945 AA.
AC Q8K1S3; Q6PFH0; Q80Y85; Q9D398;
DT 25-OCT-2004 (Rel. 45, Created)
DT 25-OCT-2004 (Rel. 45, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Netrin receptor UNC5B precursor (Unc-5 homolog B) (Unc-5 homolog 2).
GN Name=Unc5b; Synonyms=Unc5h2;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM 1), AND TISSUE SPECIFICITY.
RX MEDLINE=22239710; PubMed=12351186; DOI=10.1016/S0925-4773(02)00248-4;
RA Engelkamp D.;
RT "Cloning of three mouse unc-5 genes and their expression patterns at
RT mid-gestation.";
RL Mech. Dev. 118:191-197(2002).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RC STRAIN=C57BL/6J; TISSUE=Medulla oblongata;
RX MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
RA Nikaido I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,
RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
RA Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
RA Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,
RA Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,
RA Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
RA Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
RA Kanai A., Kawaji H., Kawasaki Y., Kedzierski R.M., King B.L.,
RA Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
RA Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,
RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
RA Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K.,
RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
RA Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,
RA Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L.,
RA Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
RA Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
RA Birney E., Hayashizaki Y.;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).

RN [3]
 RP SEQUENCE FROM N.A. (ISOFORM 2).
 RC STRAIN=C57BL/6; TISSUE=Brain;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [4]
 RP TISSUE SPECIFICITY.
 RX PubMed=12799072;
 RA Dalvin S., Anselmo M.A., Prodhon P., Komatsuzaki K., Schnitzer J.J.,
 RA Kinane T.B.;
 RT "Expression of Netrin-1 and its two receptors DCC and UNC5H2 in the
 RT developing mouse lung.";
 RL Gene Expr. Patterns 3:279-283(2003).
 CC -!- FUNCTION: Receptor for netrin required for axon guidance. Mediates
 CC axon repulsion of neuronal growth cones in the developing nervous
 CC system upon ligand binding. Axon repulsion in growth cones may be
 CC caused by its association with DCC that may trigger signaling for
 CC repulsion. It also acts as a dependence receptor required for
 CC apoptosis induction when not associated with netrin ligand (By
 CC similarity).
 CC -!- SUBUNIT: Interacts with the cytoplasmic part of DCC. Interacts
 CC with GNAI2 via its cytoplasmic part (By similarity).
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).
 CC -!- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=2;
 CC Name=1;
 CC IsoId=Q8K1S3-1; Sequence=Displayed;
 CC Name=2;
 CC IsoId=Q8K1S3-2; Sequence=VSP_011699;
 CC -!- TISSUE SPECIFICITY: Highly expressed in brain. Expressed in lung
 CC during late development. Expressed during early blood vessel
 CC formation, in the semicircular canal and in a dorsal to ventral
 CC gradient in the retina.
 CC -!- PTM: Phosphorylated on cytoplasmic tyrosine residues (By
 CC similarity).
 CC -!- PTM: Proteolytically cleaved by caspases during apoptosis. The
 CC cleavage does not take place when the receptor is associated with
 CC netrin ligand. Its cleavage by caspases is required to induce

CC apoptosis (By similarity).
 CC -!- SIMILARITY: Belongs to the UNC-5 family.
 CC -!- SIMILARITY: Contains 1 death domain.
 CC -!- SIMILARITY: Contains 1 immunoglobulin-like C2-type domain.
 CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
 CC -!- SIMILARITY: Contains 2 TSP type-1 domains.
 CC -!- SIMILARITY: Contains 1 ZU5 domain.

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DR EMBL; AJ487853; CAD32251.1; -.
 DR EMBL; AK018177; BAB31108.1; -.
 DR EMBL; BC048162; AAH48162.1; ALT_INIT.
 DR EMBL; BC057560; AAH57560.1; -.
 DR HSSP; P07996; 1LSL.
 DR MGD; MGI:894703; Unc5b.
 DR InterPro; IPR000488; Death.
 DR InterPro; IPR011029; DEATH_like.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003598; Ig_c2.
 DR InterPro; IPR000884; TSP1.
 DR InterPro; IPR008085; TSP_1.
 DR InterPro; IPR000906; ZU5.
 DR Pfam; PF00531; Death; 1.
 DR Pfam; PF00047; ig; 1.
 DR Pfam; PF00090; TSP_1; 2.
 DR Pfam; PF00791; ZU5; 1.
 DR PRINTS; PR01705; TSP1REPEAT.
 DR SMART; SM00005; DEATH; 1.
 DR SMART; SM00408; IGc2; 1.
 DR SMART; SM00209; TSP1; 2.
 DR SMART; SM00218; ZU5; 1.
 DR PROSITE; PS50017; DEATH_DOMAIN; 1.
 DR PROSITE; PS50835; IG_LIKE; 1.
 DR PROSITE; PS50092; TSP1; 2.

KW Alternative splicing; Apoptosis; Developmental protein;
 KW Immunoglobulin domain; Phosphorylation; Receptor; Repeat; Signal;
 KW Transmembrane.

FT	SIGNAL	1	26	Potential.
FT	CHAIN	27	945	Netrin receptor UNC5B.
FT	DOMAIN	27	377	Extracellular (Potential).
FT	TRANSMEM	378	398	Potential.
FT	DOMAIN	399	945	Cytoplasmic (Potential).
FT	DOMAIN	48	145	Ig-like.
FT	DOMAIN	153	242	Ig-like C2-type.
FT	DOMAIN	246	300	TSP type-1 1.
FT	DOMAIN	302	354	TSP type-1 2.
FT	DOMAIN	541	644	ZU5.
FT	DOMAIN	865	943	Death.
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FT	SITE	707	725	Interaction with DCC (By similarity).

FT	DISULFID	69	128	By similarity.
FT	DISULFID	174	225	By similarity.
FT	CARBOHYD	222	222	N-linked (GlcNAc. . .) (Potential).
FT	CARBOHYD	347	347	N-linked (GlcNAc. . .) (Potential).
FT	VARSPLIC	356	367	NQRTLNDPKSHP -> T (in isoform 2).
FT				/FTId=VSP_011699.
FT	CONFLICT	238	238	T -> A (in Ref. 2).
FT	CONFLICT	394	394	V -> E (in Ref. 2).
FT	CONFLICT	679	679	T -> S (in Ref. 2).
FT	CONFLICT	874	874	N -> D (in Ref. 2).
SQ	SEQUENCE	945 AA; 103738 MW; 80E896F0F0E06012 CRC64;		

Query Match 49.0%; Score 274; DB 1; Length 945;
 Best Local Similarity 51.9%; Pred. No. 8.6e-21;
 Matches 54; Conservative 18; Mismatches 30; Indels 2; Gaps 2;

Qy	2	SNMTYGTFFNFLGGRLMIPNTGISLLIPDAIPRGKIYEIYLTTLHKPEDVRLPLA-GCQTL	60
		: : : : : :: :: : :	
Db	542	SSSVSGTFGCLGGRLSLPGTGVSLLPNGAIPQGKFYDLYLHINKAEST-LPLSEGSQTV	600
Qy	61	LSPIVSCGPPGVLLTRPVILAMDHCGEPSDWSLRLKKQSCEG	104
		: : : : : : :	
Db	601	LSPSVTCGPTGLLLCRPVVLTVPHCAEVIAGDWIFQLKTQAHQG	644

RESULT 12

UN5D_MOUSE

ID UN5D_MOUSE STANDARD; PRT; 956 AA.
 AC Q8K1S2;
 DT 25-OCT-2004 (Rel. 45, Created)
 DT 25-OCT-2004 (Rel. 45, Last sequence update)
 DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DE Netrin receptor UNC5D precursor (Unc-5 homolog D) (Unc-5 homolog 4).
 GN Name=Unc5d; Synonyms=Unc5h4;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A., AND TISSUE SPECIFICITY.
 RX MEDLINE=22239710; PubMed=12351186; DOI=10.1016/S0925-4773(02)00248-4;
 RA Engelkamp D.;
 RT "Cloning of three mouse Unc5 genes and their expression patterns at
 RT mid-gestation.";
 RL Mech. Dev. 118:191-197(2002).
 CC -!- FUNCTION: Receptor for netrin involved in cell migration. May be
 CC involved in axon guidance by mediating axon repulsion of neuronal
 CC growth cones in the developing nervous system upon ligand binding.
 CC Axon repulsion in growth cones may be caused by its association
 CC with DCC that may trigger signaling for repulsion. It also acts as
 CC a dependence receptor required for apoptosis induction when not
 CC associated with netrin ligand (By similarity).
 CC -!- SUBUNIT: Interacts with the cytoplasmic part of DCC (By
 CC similarity).
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).
 CC -!- TISSUE SPECIFICITY: Expressed in developing limb and mammary
 CC gland.

CC -!- PTM: Phosphorylated on cytoplasmic tyrosine residues (By
 CC similarity).

CC -!- PTM: Proteolytically cleaved by caspases during apoptosis. The
 CC cleavage does not take place when the receptor is associated with
 CC netrin ligand. Its cleavage by caspases is required to induce
 CC apoptosis (By similarity).

CC -!- SIMILARITY: Belongs to the UNC-5 family.

CC -!- SIMILARITY: Contains 1 death domain.

CC -!- SIMILARITY: Contains 1 immunoglobulin-like C2-type domain.

CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.

CC -!- SIMILARITY: Contains 2 TSP type-1 domains.

CC -!- SIMILARITY: Contains 1 ZU5 domain.

CC -----

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 CC or send an email to license@isb-sib.ch).

CC -----

DR EMBL; AJ487854; CAD32252.1; -.
 DR HSSP; P07996; 1LSL.
 DR MGD; MGI:2389364; Unc5d.
 DR InterPro; IPR000488; Death.
 DR InterPro; IPR011029; DEATH_like.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003598; Ig_c2.
 DR InterPro; IPR000884; TSP1.
 DR InterPro; IPR008085; TSP_1.
 DR InterPro; IPR000906; ZU5.
 DR Pfam; PF00531; Death; 1.
 DR Pfam; PF00047; ig; 1.
 DR Pfam; PF00090; TSP_1; 2.
 DR Pfam; PF00791; ZU5; 1.
 DR PRINTS; PR01705; TSP1REPEAT.
 DR SMART; SM00005; DEATH; 1.
 DR SMART; SM00408; IGc2; 1.
 DR SMART; SM00209; TSP1; 2.
 DR PROSITE; PS50017; DEATH_DOMAIN; FALSE_NEG.
 DR PROSITE; PS50835; IG_LIKE; 1.
 DR PROSITE; PS50092; TSP1; 2.

KW Apoptosis; Developmental protein; Immunoglobulin domain;
 KW Phosphorylation; Receptor; Repeat; Signal; Transmembrane.

FT	SIGNAL	1	30	Potential.
FT	CHAIN	31	956	Netrin receptor UNC5D.
FT	DOMAIN	31	382	Extracellular (Potential).
FT	TRANSMEM	383	403	Potential.
FT	DOMAIN	404	956	Cytoplasmic (Potential).
FT	DOMAIN	52	149	Ig-like.
FT	DOMAIN	151	242	Ig-like C2-type.
FT	DOMAIN	250	304	TSP type-1 1.
FT	DOMAIN	306	358	TSP type-1 2.
FT	DOMAIN	543	645	ZU5.
FT	DOMAIN	862	939	Death.
FT	SITE	419	420	Cleavage (by caspase-3) (By similarity).
FT	SITE	706	724	Interaction with DCC (By similarity).

FT	DISULFID	73	132	By similarity.
FT	DISULFID	178	229	By similarity.
FT	CARBOHYD	115	115	N-linked (GlcNAc. . .) (Potential).
FT	CARBOHYD	226	226	N-linked (GlcNAc. . .) (Potential).
FT	CARBOHYD	351	351	N-linked (GlcNAc. . .) (Potential).
FT	CARBOHYD	379	379	N-linked (GlcNAc. . .) (Potential).
SO	SEQUENCE	956 AA; 106351 MW; DFDF07839C10C68D CRC64;		

Qy	1	TSNMTYGTFFNLGGRLMIPNTGISLLIPPDAIPRGKIYEIYLT LHKPEDVRLPLAGCQTL	60
		: : : : : : : :	
Db	543	TELRTTGVFGHLGGRLVMPNTGVSL LIPHGAIPEENSWEIYMSINQGEP-SLQSDGSEVL	601
Qy	61	LSPIVSCGPPGVLLTRPVILAMDHCGEPSD SWSLR LKKQSCEG	104
		: : : : : : : : : :	
Db	602	LSPEVTCGPPDMLVTTTPFALTIPHCADVSSEHWN IHLKKRTOQG	645

RESULT 13

```

ID      UN5D_HUMAN STANDARD; PRT; 953 AA.
AC      Q6UXZ4; Q8WYP7;
DT      25-OCT-2004 (Rel. 45, Created)
DT      25-OCT-2004 (Rel. 45, Last sequence update)
DT      25-OCT-2004 (Rel. 45, Last annotation update)
DE      Netrin receptor UNC5D precursor (Unc-5 homolog D) (Unc-5 homolog 4)
DE      (UNQ6012/PRO34692).
GN      Name=UNC5D; Synonyms=KIAA1777, UNC5H4;
OS      Homo sapiens (Human)..
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX      NCBI_TaxID=9606;
RN      [1]
RP      SEQUENCE FROM N.A. (ISOFORM 1).
RX      MEDLINE=22887296; PubMed=12975309; DOI=10.1101/gr.1293003;
RA      Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D., Brush J.,
RA      Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,
RA      Eaton D., Foster J., Grimaldi C., Gu Q., Hass P.E., Heldens S.,
RA      Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,
RA      Lewis L., Liao D., Mark M., Robbie E., Sanchez C., Schoenfeld J.,
RA      Seshagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A.,
RA      Vandlen R., Watanabe C., Wieand D., Woods K., Xie M.-H., Yansura D.,
RA      Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I.,
RA      Godowski P., Gray A.;
RT      "The secreted protein discovery initiative (SPDI), a large-scale
RT      effort to identify novel human secreted and transmembrane proteins: a
RT      bioinformatics assessment.";
RL      Genome Res. 13:2265-2270(2003).
RN      [2]
RP      SEQUENCE FROM N.A. (ISOFORM 2).
RC      TISSUE=Brain;
RA      Nakajima D., Nakayama M., Nagase T., Ohara O.;
RT      "Identification of unc5H4 gene.";
RL      Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.

```

CC -!- FUNCTION: Receptor for netrin. May be involved in axon guidance by
 CC mediating axon repulsion of neuronal growth cones in the
 CC developing nervous system upon ligand binding. Axon repulsion in
 CC growth cones may be caused by its association with DCC that may
 CC trigger signaling for repulsion. It also acts as a dependence
 CC receptor required for apoptosis induction when not associated with
 CC netrin ligand (By similarity).
 CC -!- SUBUNIT: Interacts with the cytoplasmic part of DCC (By
 CC similarity).
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).
 CC -!- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=2;
 CC Name=1;
 CC IsoId=Q6UXZ4-1; Sequence=Displayed;
 CC Name=2;
 CC IsoId=Q6UXZ4-2; Sequence=VSP_011703;
 CC Note=No experimental confirmation available;
 CC -!- PTM: Phosphorylated on cytoplasmic tyrosine residues (By
 CC similarity).
 CC -!- PTM: Proteolytically cleaved by caspases during apoptosis. The
 CC cleavage does not take place when the receptor is associated with
 CC netrin ligand. Its cleavage by caspases is required to induce
 CC apoptosis (By similarity).
 CC -!- SIMILARITY: Belongs to the UNC-5 family.
 CC -!- SIMILARITY: Contains 1 death domain.
 CC -!- SIMILARITY: Contains 1 immunoglobulin-like C2-type domain.
 CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
 CC -!- SIMILARITY: Contains 2 TSP type-1 domains.
 CC -!- SIMILARITY: Contains 1 ZU5 domain.

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DR EMBL; AB055056; BAB83663.1; -.
 DR EMBL; AY358147; AAQ88514.1; -.
 DR HSSP; P07996; 1LSL.
 DR Genew; HGNC:18634; UNC5D.
 DR InterPro; IPR000488; Death.
 DR InterPro; IPR011029; DEATH_like.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003598; Ig_c2.
 DR InterPro; IPR000884; TSP1.
 DR InterPro; IPR008085; TSP_1.
 DR InterPro; IPR000906; ZU5.
 DR Pfam; PF00531; Death; 1.
 DR Pfam; PF00047; ig; 1.
 DR Pfam; PF00090; TSP_1; 2.
 DR Pfam; PF00791; ZU5; 1.
 DR PRINTS; PR01705; TSP1REPEAT.
 DR SMART; SM00005; DEATH; 1.
 DR SMART; SM00408; IGc2; 1.
 DR SMART; SM00209; TSP1; 2.

RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Uterus endothel;
 RG The German cDNA Consortium;
 RA Poustka A., Albert R., Moosmayer P., Schupp I., Wellenreuther R.,
 RA Mewes H.W., Weil B., Amid C., Osanger A., Fobo G., Han M., Wiemann S.;
 RL Submitted (AUG-2004) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; CR749235; CAH18091.1; -.
 DR InterPro; IPR008144; Guanylate_kin.
 DR InterPro; IPR008145; Guanylt/Ca.
 DR InterPro; IPR001478; PDZ.
 DR InterPro; IPR001452; SH3.
 DR InterPro; IPR011511; SH3_2.
 DR InterPro; IPR005417; ZonOcculdens.
 DR InterPro; IPR005418; ZonOcculS1.
 DR InterPro; IPR000906; ZU5.
 DR Pfam; PF00625; Guanylate_kin; 1.
 DR Pfam; PF00595; PDZ; 1.
 DR Pfam; PF00018; SH3_1; 1.
 DR Pfam; PF07653; SH3_2; 1.
 DR Pfam; PF00791; ZU5; 1.
 DR PRINTS; PR01597; ZONOCCLUDNS.
 DR PRINTS; PR01598; ZONOCCLUDNS1.
 DR SMART; SM00072; GuKc; 1.
 DR SMART; SM00228; PDZ; 1.
 DR SMART; SM00218; ZU5; 1.
 DR PROSITE; PS50052; GUANYLATE_KINASE_2; 1.
 DR PROSITE; PS50106; PDZ; 1.
 DR PROSITE; PS50002; SH3; 1.
 KW Hypothetical protein.
 SQ SEQUENCE 1267 AA; 142571 MW; 734B3877FBCAC6FA CRC64;

Query Match 34.3%; Score 192; DB 2; Length 1267;
 Best Local Similarity 43.6%; Pred. No. 1e-11;
 Matches 41; Conservative 12; Mismatches 39; Indels 2; Gaps 1;

Qy 7 GTFNLGGRLMIPNTGISLLIPPDIAIPRGIYEIYLTLLHKPEDVRLPL--AGCQTLLSPI 64
 | || || | ||:|:| || | || : : : || :|||:
 Db 1137 GIFNSNGGVLSSIETGVSIIPQGAIPGVEQEYFKVCRDNSILPPLDKEKGETLLSPL 1196
 Qy 65 VSCGPPGVLLTRPVILAMDHCGEPPSPDSWSLRLK 98
 | ||| |: :|| | : || :|| || ||
 Db 1197 VMCGPHGLKFLKPVELRLPHCASMTPDGWSFALK 1230

RESULT 15

O97758

ID O97758 PRELIMINARY; PRT; 1769 AA.
 AC O97758;
 DT 01-MAY-1999 (TrEMBLrel. 10, Created)
 DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE ZO-1 MDCK.
 GN Name=ZO1-MDCK;
 OS Canis familiaris (Dog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.

```

OX      NCBI_TaxID=9615;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      STRAIN=breed: Cocker Spaniel;
RX      MEDLINE=99196918; PubMed=10094817; DOI=10.1006/excr.1999.4392;
RA      Gonzalez-Mariscal L., Islas S., Contreras R.G., Garcia-Villegas M.R.,
RA      Betanzos A., Vega J., Diaz-Quinonez A., Martin-Orozco N.,
RA      Ortiz-Navarrete V., Cerejido M., Valdes J.;
RT      "Molecular characterization of the tight junction protein ZO-1 in MDCK
RT      cells.";
RL      Exp. Cell Res. 248:97-109(1999).
CC      -!- SIMILARITY: Contains 3 PDZ/DHR domains.
DR      EMBL; U55935; AAD11529.1; -.
DR      HSSP; P31016; 1JXO.
DR      GO; GO:0005923; C:tight junction; IEA.
DR      GO; GO:0005515; F:protein binding; IEA.
DR      InterPro; IPR008144; Guanylate_kin.
DR      InterPro; IPR008145; Guanylt/Ca.
DR      InterPro; IPR001478; PDZ.
DR      InterPro; IPR001452; SH3.
DR      InterPro; IPR011511; SH3_2.
DR      InterPro; IPR005417; ZonOcculdens.
DR      InterPro; IPR005418; ZonOcculS1.
DR      InterPro; IPR000906; ZU5.
DR      Pfam; PF00625; Guanylate_kin; 1.
DR      Pfam; PF00595; PDZ; 3.
DR      Pfam; PF07653; SH3_2; 1.
DR      Pfam; PF00791; ZU5; 1.
DR      PRINTS; PR01597; ZONOCCLUDNS.
DR      PRINTS; PR01598; ZONOCCLUDNS1.
DR      SMART; SM00072; GuKc; 1.
DR      SMART; SM00228; PDZ; 3.
DR      SMART; SM00326; SH3; 1.
DR      SMART; SM00218; ZU5; 1.
DR      PROSITE; PS50052; GUANYLATE_KINASE_2; 1.
DR      PROSITE; PS50106; PDZ; 3.
DR      PROSITE; PS50002; SH3; 1.
SQ      SEQUENCE      1769 AA; 197606 MW; 181E9F36CEBC96EF CRC64;

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Query Match 34.3%; Score 192; DB 2; Length 1769;
Best Local Similarity 43.6%; Pred. No. 1.5e-11;
Matches 41; Conservative 12; Mismatches 39; Indels 2; Gaps 1;

```
Qy      7 GTFNFLGGRLMIPNTGISLLIPPDAIPRGKIYEIYLTLHKPEDVRLPL--AGCQTLLSPI 64
        | || || |   ||::|| ||| |   || : :   : ||   :||||:
Db     1639 GVFNNGGVLSSIETGVSIIPQGAIEGVEQEYFKVCRDNSILPPLDKEKGETLLSPL 1698

Qy     65 VSCGPPGVLLTRPVILAMDHCGEPSDWSLRLLK 98
        | ||| |:   :|| | : ||   :|| || ||
Db    1699 VMCGPHGLKFLKPVELRRLPHCASMTPDGWSFALK 1732
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Search completed: March 1, 2005, 09:03:41
Job time : 21.025 secs